Requestor's Name:		Serial Number:
Date:	Phone:	Art Unit:
Search Topic: Please write a detailed statement of sear terms that may have a special meaning, please attach a copy of the sequence. Yo	Give examples or relevent c	ly as possible the subject matter to be searched. Define any itations, authors, keywords, etc., if known. For sequences, broadest and/or most relevent claim(s).

FOR OFFICIAL USE ONLY

STAFF USE ONLY

Date completed:	Search Site	Vendors
Searcher: MARIC	STIC	IG-MPRCH
Terminal time:	CM-1	STN
Elapsed time: 10	Pre-S	Dialog
CPU time:	Type of Search	APS
Total time:	N.A. Sequence	Geninfo
Number of Searches:/	A.A. Sequence	SDC
Number of Databases:	Structure	DARC/Questel
	Bibliographic	Other

Best Available Copy

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n.a. . n.a. database search, using Smith-Waterman algorithm MPsrch_nn

MasPar time 820.34 Seconds 978.029 Million cell updates/sec Thu Nov 6 10:15:18 1997; Run on:

Fabular output not generated.

>US-08-842-827-1 (1-1563) from US08842827.seq 1563 1 CCTGTGGGAGAGAGCGCGG. Description: Perfect Score: N.A. Sequence: Comp: Title:

......GGTTTTTTTTTTTTTTTTTTTTT

TABLE default Gap 6 Gap Scoring table:

707517 seqs, 256659390 bases Searched:

Dbase 0; Query 0

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STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

EST-STS Database:

1.EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 15:EST8 10:EST10 11:EST10 11:EST10 11:EST10 11:EST10 11:EST10 12:EST10 12:E

Database:

162:EST162 163:EST163 167:EST167 168:EST168 172:EST172 173:EST173

179:EST179 184:EST184 189:EST189 194:EST194 175:EST175 176:EST176 177:EST177 178:EST178 180:EST180 181:EST181 182:EST182 183:EST183 185:EST185 186:EST186 187:EST187 188:EST188 190:EST190 191:EST190 192:EST197 198:EST193 195:EST195 196:EST196 197:EST197 198:EST193

Variance 2.893; scale 4.080 Mean 11 804; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	: H97570 587 bp mRNA EST 12-DEC-1995	06.sl Homo sapiens cDNA clone 260627 3'.		455		human clone-260627 primer-m13 -40 forward library-Soares melan
	H97570 587 b	yx03b06.sl Homo sap	H97570	g1118455	EST.	human clone-260627
RESULT 1	LOCUS	DEFINITION	ACCESSION	OIN	ω	SOURCE

human clone=260627 primer=m13 -40 forward library=Soares melanocyte

a

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/note="Organ: uterus; Vector: pr773-Pac; Site_1: Not I; Site_2: Eco RI; lat strand cDNA was primed with a Not I oligo(dT) primer [5' AACTGGAAGAATTGGGGGCGCCTTTTTTTTTTTTTTT 3'] AACTGGAAGAATTGGCGGCCGCTTTTTTTTTTTTTTTT 3'] (Pharmacla), dlgested with Not I and cloned into the Not and Eco RI sites of the modified pr773 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                         ANA 3085 545 bp mRNA EST 04-SEP-1996 48602.rl Soares pregnant uterus NbHPU Homo sapiens CDNA Clone A86027 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Seg primer: -28Mls rev2 from Amersham
High quality sequence stop: 485.
Location/Qualifiers
       1186 TGATTGCTCGGATAGTGATTCCCAGTTGTTGGTGTTTCATGCAGAGTTGTATGAGAGTCC 1127
                                                                                             1126 TCCTCTTTCTTTCTTTAAAAGAAGTTCTTTCTTTGAAGAAATCCGATACATATACAGCA 1067
                                                                                                                                                                 420 tcctcctttcctttctttaaaagaagttctttccttgaagaaatccgatacatatacagca 479
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulfman,M., Kucaba,T., El.M., Lennon,C., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                           480 actaatattgcaaccagagctccctgaatgagtccagtcaacacatcgctcccagtgggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashIndwerck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.00e+00;
0; Mismatches 3;
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/lab_host="DH10B"
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larity 98.7%;
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Eukaryotae: Metazoa: Eumetazoa: Bilateria; Coelomata:
Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osteichthyes;
Sarcopterygii; Choanata: Tetrapoda: Amniota: Mammalia: Theria:
Eutheria: Archonta: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 587)
Hillari., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Rucaba, T., Le, M., Lenon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
High quality sequence stops: 351
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1485 TATTACATACATGTTTATACATAAGCATTACATTTTTTAATAAAATGTATACAGGTGG 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1425 GCCACTGTTTTGGTGGAAGGCTTGGAGTTTTTTAATGAGTTTAGAGCTATTAGATAACC 1366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1245 ATTTTCCTTTAGAAAACAGGCCAGCTTCACCTGGGCACCCTGCTGCCTTTCAAGGCTGG- 1187
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 0.00e+00;
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WashU-Merck EST Project
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Best Local Similarity 96.6%;
Matches 565; Conservative
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Fax: 314 286 1810
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/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not
                                                                                                                                                                                                                                             32.4%;
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Matches 533; Conservative
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AA036943
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Location/Qualifiers
1..552
                          1179 AGCAATCACCAGCCTTGAAAGGCAGCAGGTGCCCAGGTGAAGCTGGAAGCTGCCTGTTTTCTAAA 1238
                                                                                                                                    240
                                                                                                                                                                                     241 agcaatcaccagcettgaaaggcagcaggtgeecaggtgaagetggeetgttttetaaa 300
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollenan,M., Ruababa,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffin,L., Rohlfing,T., Scares,M., Parsons,J., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                         acagtgcccacctgtatacatttttattaaaaa-tgtaatgcttatgtataa-catgt
939 CCCACACTGCAATTTGGTCTTGTTGCCGTATCCATTTATGTGGGCCTTTCTCGAGTTTCT
                                                                              1418 ACAGTGCCCCACCTGTATACATTTTTATTAAAAATGTAATGCTTATGTATAAACATGT
                                                                                                                                  181 aaagaagaagacteteatacaactetgeatgaaacaccaacaactgggaateactateeg
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WashU-Merck EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis,
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
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double-stranded CDNA was ligated to Eco RI adaptors (Pharmacta), digested with Not I and cloned into the Not I and Eco RI stres of the modified prival vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

/clone=472051
/clone=1205-"Soares pregnant uterus NDHPU"
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zd38a11.s1 Soares fetal heart NbHH19W Homo sapiens CDNA clone
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                        complement(<1..>552)
105 c 110 g
                                                                                                                                              /sex="female"
/dev_stage="adult"
/lab_host="DH10B"
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/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
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double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the No
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
/clone="466027"
/clone=11b="Soares pregnant uterus NDHPU"
                                                                                                                                                                                                                                                                 AAU40858 465 bp mRNA EST 30-AUG-1996
2K48b02.31 Soares pregnant uterus NbHPU Homo sapiens CDNA Clone
AA6027 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 354.
Location/Qualifiers
1.465
                                          421 cagagetecetggaatgagtecagteaacategetecagtggtgttttataateateagaaa 480
                     361 tttaaaagaagttetttetttgaagaaateegataeatacageaaetaatattgeaae 420
                                                                                                                        1052 CAGAGCTCCCTG-AATGAGTCCAGTCAACACGCTCCCAGTGGTTTTTATAATCAGAAA 994
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Bukaryotes, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( (bases 1 to 465)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                             481 occogagaaaggocacataaatggatacggcaacaagaccaaattgcagtgtgggg 536
                                                                                                                                                                                                       Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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Pred. No. 0.00e+00;
0; Mismatches 3;
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/lab_host="DH10B"
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Washbuyerck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Exa: 314 286 1800
Exa: 314 286 1800
Exa: 314 286 lano
Exail: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (inf@@imago.llnl.gov) for further information.
Insert Length: 634 Std Error: 0.00
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               1 (bases 1 to 546)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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/clone_11b="Soares fetal heart NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="0H10B (ampicillin resistant)"
complement(<1..546)
105 c 121 g 159 t 2 other
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2a43909.rl Soares fetal liver spleen INFLS Homo sapiens CDNA clone
295360 5' similar to WP:T28D9.3 CE02068 ;.
1366
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                                                                                                              300
                                                                                                    240
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Ritkin,L., Rohlfing,T., Soares,M., Parsons,J., Ritkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                181 actgagttaaaggtaactatgtacacacaaagtgtgcatccaagaggcatagcagcag
                                                                                                                                                                                                  atttcctttagaaaacaggccagcttcacctgggcaccctgctgcctttcaaggctggt
                                                                                                                                                                                                                        1245 ATTITCCTTTAGAAACAGGCCAGCTTCACCTGGGCCACCTGCTGCTTTCAAGGCTGGT
                                                                                                                                                                                                                                                     gattgctcggatagtgattcccagttgttggtgtttcatgcagagttgtatgagagtcct
                                                  ggcactgttttggtggaaggcttggagtttttttaatgagtttagagctattagataacc
                                                                                                                                                                                                                                                                             GATTGCTCGGATAGTGATTCCCAGTTGTTGGTGTTTCATGCAGAGTTGTATGAGAGTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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High quality sequence stop: 339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project
Unpublished (1995)
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SOURCE

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N31U47 490 bp MRNA EST 10-JAN-1996
YSS1NO7.r1 Homo sapiens CDNA clone 265309 5' similar to WP:T28D9.3
N31O47
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                                                                                                                                                                                                                            ctgtctgtttactgtaaccttttgcactcaaattcctttatcaggaataactacatagcc 120
                                                                                                                                                                                                                                                                                                                                                                                        agattggtcaaaaatcaactgcaagcgatggttacattgaatactacatatgtcgaggga 300
                                                                                                                                                                                                                                                                                                                                                                                                                                           atgcagaaagagttaaggaaggcaggttgtccttctattcaggccactcttcgttttcca 360
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                                                                                                                                                                                                                                                                                                         1 cgttattaggtggaataatcattccattcagtattatccgttattattcttggagaaacc
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ო
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone-"295360"
/clone_lib-"Soares fetal liver spleen INFLS"
/sex-"male."
/dev_atge="20 week-post conception fetus"
/lab_host-"DH10B (ampicillin resistant)"
                                                                                                                                                 Indels
                                                                                                                     Score 448; DB 114;
Pred. No. 0.00e+00;
0; Mismatches 1;
                                                                              152
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99.2%;
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102 c
                                                                                                                                                467; Conservative
                                                                                                                                  Similarity
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COMMENT

ORIGIN

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Contact: Wilson RK
WashU-Warck EST Project
WashU-Warck EST Project
WashU-Warck EST Project
WashU-Warsity School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 634 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 328.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1012 ACTGGAGCGATGTGTTGACTGGACTCATTCAGGGAGCTCTGGTTGCAATATTAGTTGCTG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 tatatgtatcggatttcttcaaagaacttctttaaagaagaagaaggaggact 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 actggagcgatgtgttgactggactcattcagggagctctggttgcaatattagttgctg 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 ctcatacaactctgcatgaaacaccaacaactgggaatcactatccgagcaatcaccagc 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  892 ITTATCTTCAAGCCAGGATGAAGGGAGACTGGGCAAGACTCTTACGCCCCACACTGCAAT 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 tttatcttcaagccaggatgaaggagactgggcaagactcttacgccccacactgcaat 61
                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrate; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (2018) 1 to 446)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollann,M., Kucaba,T., Ele,M., Leanon,G.,Marra,M. Parsons,J., Rhitin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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/clone_11b="Soares fetal heart NbHH19W"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 406; DB 171;
Pred. No. 0.00e+00;
0; Mismatches 1;
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/lab_host="DH10B (ampicillin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Homo sapiens"
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l Similarity 98.9%;
431; Conservative
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                                                                                                                                                                                                 High quality sequence stops: 385
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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3438a11.:1 Soares fetal heart NDHH19W Homo sapiens cDNA clone
W67666
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Irevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                               Contact: Wilson RK
Washbu-Merck ESP Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                             Length 490;
                                                                                                                                                                                                                                                                                                                                                             3 others
                                                                                                                                                                                                                                                                                                                                                                                                             Score 414; DB 92;
Pred. No. 0.00e+00;
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                Wilson, R.
The WashU-Merck EST Project
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Best Local Similarity 97.1%;
Matches 476; Conservative
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REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/organism="Homo sapiens"
/organism="Hom
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Insert Length: 728 Std Error: 0.00
Seq primer: mob.REGA+ER
High quality sequence stop: 435.
High quality sequence stop: 435.
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          1216 GTGAAGCTGGCCTGTTTTCTAAAGGAAATGATTGCCACAAGGCAAGAGGATGCATCTTT 1275
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                                                                                                                                                                                                                                           181 aaagaacttottttaaagaaagaaagaagagaggactotoatacaactotgcatgaaacac 240
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                                                                                                                                                                                                                                                                                                                                                                         241 caacaactgggaatcactatccgagcaatcaccagccttgaaaggcaggagggtgcccag 300
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                            121 tcattcagggagctctggttgcaatattagttgctgtatatgtatcggatttcttcaaag
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The WashU-Merck EST Project
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WashU-Merck EST Project
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2240fil.rl Scares fetal liver spleen INFLS Homo sapiens cDNA clone
295053 5' similar to contains element MER12 repetitive element ;.
W01275
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Washb-Merck EST Project
Washbigton University School of Medicine
Mashbigton University School of Medicine
Mashbigton University Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPrimer
High quality sequence stop: 429.
Location/Qualifiers
                                                                                                  1192 CTTGAAAGGCAGCAGGTGCCCAGGTGAAGCTGGCCTGTTTTCTAAAGGAAAATGATTGC 1251
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rithin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
6; Indels 10;
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/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 0.00e+00;
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Source

FEATURES

BASE COUNT ORIGIN

mRNA

Matches

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pT7T3

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91027103
EST.
human clone=211821 primer=M13RPl library=Soares fetal liver spleen
1NFGs vector=pT773D (Pharmacia) with a modified polylinker
host=DH10B (amplcillin resistant) RSitel=Pac I RSite3=Eco RI Liver
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This clone is avallable royalty-free through LLNL; contact the
MAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 728 Std Error: 0.00
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YF82fil.rl Homo sapiens cDNA clone 211821 5'

H68363
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Pred. No. 0.00e+00;
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                                                                     Seq primer: mob.REGA+ET
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Local Similarity 98.3%;
nes 415; Conservative
      Fax: 314 286 1810
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vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo."
/clone="322938"
/clone="11b" Soares senescent fibroblasts NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="bH108 (ampicillin resistant)"
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Rudaba,T., Le,M., Lennon,C., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Raterston,R., Williamson,A., Wohldmann,P. and
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WashU-Merck EST Project
WashUngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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                                                                                                                                                            Length 456;
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The Washu-Merck EST Project
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WashU-Merck EST Project
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Best Local Similarity 97.4%;
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Aminiota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
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1 (bane, M., Hultman, M., Rucaba, T., Eliston, K., Hawkins, M.,
Hollman, M., Hultman, M., Kucaba, T., E., M., Lenon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 379
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                Contact: Wilson RK
Washindwerck E3T Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 0.00e+00;
0; Mismatches 4
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/clone="211821"
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1 Similarity 97.1%;
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/note-"Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 11; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACTGGAAGAATTGGGGGCGCTTTTTTTTTTTTTTTT 3'),
double-stranded cDNa was ligated to Eco RI adaptors
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
471 bp mRNA EST 10-DEC-1996
Soares pregnant uterus NbHPU Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28Mi3 rev2 from Amersham
High quality sequence stop: 377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vetebrata: Butheria; Primates; Catarrhini; Hominidae: Homo. [ (bases 1 to 411) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riftin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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/sex="female"
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Pred. No. 0.00e+00;
0; Mismatches 1;
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The WashU-Merck EST Project
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/lab_host="DH10B"
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human clone=240696 primer=M13RP1 library=Soares fetal liver spleen
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Anniota; Mammalia; Theria;
Eutheria; Archonta; Primaches; Catarrhini; Hominidae; Homo.
1 (bases 1 to 479)
Hillari, Clark, M., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., E., M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
WashUnderck EST Project
WashUnderck EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
High quality sequence stops: 364
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                1288 CAAGCCTTTAAAGACTTCTGCTGCTGATA-TGCCTCTTGGATGCACACTTTGTGTGTACA 1346
                                                                                                                                                                                                                                                                                                                                                                                                                            1228 TGITITCTAAAGGAAAATGATIGCCACAAGGCAAGAGGATGCAICTITCTTCCTGGTGTA 1287
                                                                                                                                                                                                                                   121 aagaaagaaaagaaggacteteatacaactetgcatgaaacaccaacaactgggaate 180
                                                                                                                                                                                                                                                                                                            181 actatenecagegeaateaceageettgaaaggeageageaggtgeeeaggtgaagetggee 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 tgttttctaaaggaaaatgattgccacaagn-aagaggatgcatcttcttcctggtgta 299
                                                                              1 gagtttctgattataaacaccactggagcgatgtgttgactggactcattcagggagctc 60
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N
        Length 415;
                                           Indels
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yu86c1.rl Homo saplens cDNA clone 240696 5'. 
H90961 
G1081391
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m
  Score 376; DB 151;
Pred. No. 0.00e+00;
0; Mismatches 3;
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Matches 408; Conservative
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zb63f08.rl Soares fetal lung NbHL19W Homo sapiens CDNA clone 308295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 773 Std Error: 0.00
Seq primer: mob.REGA+ET.
1178 GAGCAATCACCAGCCTTGAAAGGCA-GCAGGGTGCCCA-GGTGAA-GCTGGCCTGTTTTC 1234
                                                                                                                                                                                                                                 1235 TAAAGGAAATGATTGCCACAAGGCAAGAGG-ATGCATCTTTCTT-CCTGG-TGTACAAG 1291
                                                                                                                                      366
                                                                                                                                                                                                             Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo. I (bases 1 to 415)
Hillier, Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hutman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Unpublished (1995)
                                                                                                                                307 gagcaatcaccagcettgaaaggcaagcagggtgeecaaggtgaatgetggeetgtttte
                                                          abaagaaggagteteteatacaactetgeatgaaacaceaacaactgggaateactatee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashNowherck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                          1292 CC--TTTARAGAC-TTCTGCTGCTGCTGATATGCCTCTTGGA 1327
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Location/Qualifiers
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                                                                                           1 atttggtctngttgccgtatccatttatgtgggcctttctcgagtttctgattataaaca 60
                                                                               Gaps
                                                               Score 377; DB 74; Length 479;
Pred. No. 0.00e+00;
0; Mismatches 2; Indels 7;
                                            5 others
                                            142 €
                    /organism="Homo sapiens"
/clone="240696"
<1..>479
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Matches 420; Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Thu Nov 6 09:39:11 1997; MasPar time 1301.12 Seconds 1319.331 Million cell updates/sec Run on:

>US-08-842-827-1 (1-1563) from US08842827.seq 1563 Tabular output not generated. Description: Perfect Score: N.A. Sequence: Title:

1 CCTGTGGGAGAGAGCGCCGG.

TABLE default Gap 6 Scoring table:

362067 seqs, 549138275 bases x 2 Dbase 0; Query 0 .. STD Searched: Nmatch

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

embl-new3 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC

genbank99

Database:

18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2 31:GEN3 32:BCT6 33:ETT1 29:GEN1 30:GEN2 31:GEN3 32:BCT6 33:ETT02 28:BCT11 29:GEN1 30:GEN2 31:GEN3 32:BCT6 33:ETT02 28:BCT11 29:GEN1 30:GEN2 31:ETN02 31:ETN02 31:ETN02 31:ETN02 31:ETN02 31:ETN02 31:ETN02 45:ETN02 61:ETN02 61:ETN02 61:ETN02 61:ETN02 61:ETN02 61:ETN03 62:ETN03 63:ETN03 63:ETN03

Database:

genbark-new3 106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2 118:ROD 119:SYN 120:UNA 121:VRL u-embl50_99 122:part1

Database:

Variance 6.210; scale 1.921 Mean 11.930; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Pred. No.	House mouse; Musculus 0.00+00 Mus musculus (clone H 8.00e-29' 2 Human mRNA for KIAA00 1.11e-71	R.norvegicus mRNA for 2.5 Human clone 23748 mRN 1.2 Sequence 5 from paten 2 6	Sequence 5 from paten 3.2	Drosophila melanogast 1.4	Drosophila melanogast 1.4	B.taurus mRNA for cyc 1.5 R.norvegicus P2X mRNA 1.5	C. aureus GNAT2 gene 1.5	D.obscura A+T-rich re 5.1 Mouse Murrl mRNA. exo 5.	Mouse Murrl mRNA, exo 5.1	L. polyphemus mRNA for 5.1 Dictyostelium discoid 5.1	Zw=glucose-6-phosphat 5.1 Plasmodium chabaudi d 5.1 Plasmodium falciparum 5.1	R.norvegicus mRNA for 5.1 Dictyoselium discoide 5.1	Human DNA sequence ** 5.	O.sativa mRNA for T23 1.6 Brassica nabus antifu 1.6	Yeast cytochrome c ox 1.6 Dictyostelium discoid 1.6	Myrmecia pilosula HIB 1.6	Plasmodium falciparum 1.6 H.sapiens mRNA for Ar 1.6	Dictyostellum discold 1.6 Panulirus argus gluta 1.6	ous nytta magnipeptinata D.discoideum gp80 gen 1.6 Plasmodium falciparum 1.6 Plasmodium falciparum 1.6	MENTS	mRNA ROD 03-OCT-1996 mesticus kidney mRNA for Phosphatidic acid is.	tase; 35-kDa phosphatidic acid	to mRNA. . eukaryotes; Metazoa; Chordata; entia; Sciurognathi; Muridae; Murinae;	to the DDBJ/EMBL/GenBank databases. Hideo University School of Medicine, Department of South:1, Sapporo, Hokkaldo 060, Japan cc.sapmed.ac.jp, Tel:011-611-2111(ex.2290),
DB ID								- 0	-				_		SCO	MPU	HSA	19 DDUS3884 14 PNLGTSYN	44 PFU31 44 PFU31 44 PFU31	ALIGNMENT	1212 bp mRR Musculus domes complete cds.	1 phosphatase;	cDNA drial	112) 1. (4-1996) to sedical Un st-17, So
Length				4601								3774		347					3700 3700 7989 9353		121; use; Musc ase, com	idic acid		Mus. 1 (bases 1 to 1212) Kanoh, H. Direct Submission Submitted (10-APR-1996) Kanoh, Sapporo Medical (BioChemistry; West-17, § (E-mail:Kanoheserpent.cc Fax:011-612-5861)
Query Match	36. 26.	7 9 7	1010		, vi -	بنب		ا با با	اجا جا	بنب	નં નં નં	i	-ii		i -i -i	ر ا		-	1111		1 D84376 1 House mouse; M phosphatase, c D84376	1487872 hosphat	Mus musculus Mus musculus Eukaryotae; m	Mus. 1 (base Kanoh, H. Direct S Submitte Kanoh, S Biochemii (E-mail:
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llarity 86.8%;
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//db_xred="PiD:gid81873"
//db_xred="PiD:gid81873"
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SDIKHHWSDVYVGLIQGAAMAILVALKVGSFRKOTHSYKERKEEDPHTTLHEFASSRN
2 (bases 1 to 1212)

Kai.M., Wada,I., Imai.S., Sakane,F. and Kanoh,H.
Identification and cDNA cloning of 35-KDa phosphatidic acid
phosphatase (type 2) bound to plasma membranes. Polymerase chain
reaction amplification of mouse H202-inducible h1c53 clone yielded
the cDNA encoding phosphatidic acid phosphatase
J. Blol. Chem. 271 (31), 18931-18938 (1996)
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Pred. No. 0.00e+00;
0; Mismatches 124; Indels
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                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                              /evidence-experimental
                                                                                                                                                   /tissue_type="kidney"
287..1138
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/product="hydrogen peroxide-inducible protein" /db_xref="pip:giloli00" /rranslation=ARASLELARPVOEGTGORRPIGRDEPALREGAPEAGIAASTVVK ESRKHCSVGRRPIOTGPGPCSROSKRLAVAMGRRHPEGGALGIGYLDRRCLFLPPLAP
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KEDTIPTALLGGIVIPFCIJWSGIGSESLSVYFVNLBSNSFWORVIATIYKAVGAFLE
GVSASOSLTDIAKTIGSLRPHFLALCNPDMSKINCSBOYTEDVICGGREEKVREGRL
SFGGTLFILYVLHAVCRTLSSRRLARLLRPMLQFGLIAFSIYVGLFSSV" by hydrogen ä Muridae; MUSHPIP 1490 bp mRNA ROD 11-JAN-1996 Mus musculus (clone HIC-53) hydrogen peroxide-inducible protein 1049 ICTGGTTGCAATATTAGTTGCTGTATTGTATCGGATTTCTTCAAAGAAGAACTTCTTT 1108 ccagccggtgaccatgttcgacaagacgcggctgccgtacgtggcctccagatgtgatttg 380 440 448 500 560 329 CCGGGCAGAGCCATGTITGACAAGACGCGGCTGCCGTACGTGGCCCTCGATGTGCTCTG 388 Gaps RNA 994 tgctatggctatactggttgctttgtatgtatccgatttcttcaaggacacacattctta aggaatattetgtaatgatgacteeateaagtaecettaeaaggaagaeaceataeetta tgccttattaggtggaatagtcattccattctgtattatcgttatgagtattggagaatc Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; 91161099 1161099 peroxide; hydrogen peroxide-inducible protein. Mus musculus (clone: HIC-53) embryo calvariagag cDNA to Mus musculus (Egawa.K., Yoshiwara,M., Shibanuma,M. and Nose,K. Isolation of a novel ras-recision gene that is induced leperatide from a mouse osteoblastic cell line, MC3T3-E1 FEBS Lett. 372 (1), 74-77 (1995) ä Length 1490; 74; Indels 1054 caaagagaaaggaagaggatccacacacgactctccatgaaac 1098 1109 TAAAGAAAAAAAGAGGAGTCTCATACAACTCTGCATGAAAC Pred. No. 8.00e-297; 0; Mismatches 74;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (22-MAR-1994) to the DDBJ/EMBL/GenBank databases.
Nobuyuki Miyajima, Kazusa DNA Research Institute, Laboratory of
Genome Information; 1532-3 Yanauchino, Kisarazu, Chiba 292, Japan
(E-mail:miyajima@kazusa.or.jp, Tel:0438-52-3917, Fax:0438-52-3918)
2 (bases 1 to 3353)
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509 IGCGITATTAGGIGGAATAAICATICCATICAGIAITAICGITATIAITCIIGGAGAAAC 568
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                          741 agactggtcaaaaatcaactgcagtgatggctatattgaggactacatatgtcaagggaa
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Human mRNA for KIAAO052 gene, partial cds.
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/sex="male"
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0438-52-3918,
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Kisarazu, Chiba 292
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(bases 1 to 2206)
Barlla,D., Plateroti,M., Nobili,F., Muda,A.O., Xie,Y., Morimoto,T.
and Percozzi,G.
The Dri 42 gene, whose expression is up-regulated during epithelial
differentiation, encodes a novel endoplasmic reticulum resident
/db_xref="PID:g473933"
//translation="Likeradargdelesypegdstythagtkidkekddkgkwkgppgs
//translation="Likeradargdelesypegdstyckrprieesitedisladidapr
ykvqsvetveggthevalpaeedylplkprvgkaaketpfflidaforealqcvdnngs
                                                                                                              VIVSAHTSAGKTVCAEYATALALREKORVIFTSPIRALSNOKYRBYEEFODVGLATG
DVTINPTASCLVATTEILRSMLYRGSEVAREVAWVIFDEIHYMRDSERGVVWEEFIIIL
LPDNVHYVFLSATIPNARQFAEWICHLHKOPCHVIYTDYRPTPLQHYIFPAGGDGLHL
                                                                                                                                                                                                    VVDENGDFREDNFNTAMQ<sup>V</sup>LRDAGDLAKGDQKGRKGGTKGPSNVFKIVKMIMERNFQP
VITYSFSKRCDCRXALQM*KLDFNTDBEKKWYBEPFSNAIDCLSDEDKLEDQVBTVLP
LLKRGITHHGGLLPILKET EILFSEGLIKALFATETRAMGINNPARYUFTNARKF
DGKDFRWISSGETIQMSGRAGRRGMDDRGIVILMVDEKMSPTIGKQLLKGSADFUNSA
                                                                                                                                                                                                                                                                                                                      FHLFYNMYLNILLRVEELNPEYMLEKSFYOFOHYRALPGVVEKVKNEEDYNKIVIPNE
ESVVIYYKIROOLAKLGKEIEEYIHKPKYCLPFLOPGRLVKVKNEGDDFGWGVVVNFS
KKSNVKPNSGELDPLYVVEVLLRCSKESLKNSATEAAKPAKPDEKGEMOVVPVLVHLL
                                                                                                                                                                                                                                                                                                                                                                                                           SAISSVRLYIPKDLRPVDNRQSVLKSIQEVQKRFPDGIPLLDPIDDMGIQDQGLKKVI
QKVJARPEHRYSHPLHNDPNLETVYTLCEKKSTDCNRY"
2512. :3353
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Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 1.11e-71;
0; Mismatches 0; Indels 0
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J. Biol. Chem. 271 (47), 29928-29936 (1996)
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410..1348
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Norway rat.
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/dev_stage="adult"
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/codon_start=1
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Best Local Similarity 100.0%;
Matches 130; Conservative
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/organism="unknown"
                                   /sex="female"
/dev_stage="infant"
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               /clone-"23748"
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1 Similarity 62.8%;
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Best Local Similarity 17.1%;
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/product-"ER transmembrane protein"
/db_xref-"PID:e283078"
/db_xref-
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Andersson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and Gibbs,R.A. A double adaptor' method for improved shotgun library construction Anal. Blochem. 236 (1), 107-113 (1996)
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S930, Houston, TX 77030, USA
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Riozfrente,J.Y., Wentland,M.A., Lennon,G. and
Large Scale Concatenation cDNA Sequencing
Unpublished
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Pred. No. 2.52e-57;
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Direct Submission

Submitted (22-NOV-1996) Molecular and
College of Medicine, One Baylor Plaza
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Best Local Similarity 64.5%;
Matches 247; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   972 gootcottotocatgtacactatgotgtatttggtgctatacotgcaggcccgcttcact 1031
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                                                                                                      851
                                                                                                                                                                                                 852 agtgtctgcaaccctgatttcagccagatcaactgctctgaaggctacattcagaactac 911
                                                                                                                                                                                                                                                                                                  912 agatgcagaggtgatgacagcaaagtccaggaagccaggaagtccttcttctctggccat 971
                                                                                                                                                 675 AGTCAGTCCCTGACTGACATTGCCAAGTATTCAATAGGCAGACTGCGGCCTCACTTCTTG 734
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                                                     Gaps
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Bennett.A., Labavitch,J.M., Powell,A. and Stotz,H.
Bennett.A., Labavitch,J.M., Powell,A. and Stotz,H.
Bennett.A., Labavitch,J.M., Powell,A. and Stotz,H.
Bennett. S 5569830-A 5 29-OCT-1996;
                                                                                                                                                                                                                                                                                                                                  792 agceagtettteacagacattgecaaagtgtecatagggegeetgegteeteattettg
                                                                                                                                                                                                                                               735 GATGTTTGTGATCCAGATTGGTCAAAATCAACTGCAGCGATGGTTACATTGAATACTAC
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  Length 1444;
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                                                   0; Mismatches 155; Indels
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Pred. No. 2.60e-08;
Score 102; DB 78;
Pred. No. 1.29e-50;
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Sequence 5 from patent US 5569830.
128278
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Matches

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/product-"M2 (small) subunit of ribonucleotide reductase"
/db_xref="PTD:g10342"
/db_xref="SHISS-PROT:P07201"
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TPLKQEIKPVVKKSQQVEPLIADNPRRFVVLPIQYHDIWKMYKKAEASFWTAEEVDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENIHSEMYSLLIDTYIKDPOERDFLENAIETMPCVKEKADWAMRNINDDSSSYAËRVV
ARAAVEGIFESGSFASIFMLKKRGIMPGLTFSBRLISRDEGLHCDFACLMFSHLVNKP
SQERIHQIIDEAVKIEQVFLTBALPORLIGHNCDLANGYIEFVAFLLLELKCDKLYN
KENPFDFMEHISLEGKTINFFERRVGEYQKMGVMSGGNTGDSHAFTLDADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDMAHWESLKKEEKHFISHVLAFFAASDGIVNENLVERFSKEVQVTEARCFYGFQIAM
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1 (bases 1 to 4601)

Lewis,D.L., Parr,C.L., Farquhar,A.L. and Kaguni,L.S.
Sequence, Organization and Evolution of the A+T Region of Drosophila melanogaster Mitochondrial DNA

MOI. Biol. Evol. 11, 523-538 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="mt:ori"
/note="Description: mitochondrial origin; repeat I-A"
/rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-NOV-1990) Hunt T., Standart N., Department of Biochemistry, Tennis Court Road, Cambridge, CB2 10W, England E, (bases 1 to 172)
Standart, N., Dale, M., Stewart, E. and Hunt, T. Genes Dev. 4 (1990) In press
Forms a complex with the product of the large MI subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMU11584 4601 bp DNA INV 23-JUL-1
Droscphila melanogaster Oregon-R mitochondrial A+T region.
U11584
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East Lansing, MI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-JUN-1994) Laurie S. Kaguni
Blochemistry, Michigan State University,
48824-1318, USA
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Pred. No. 4.10e-03;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                 /dev_stage="cocyte"
/cell_type="cocyte"
96..1250
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1..4601
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/dev_stage="embryo"
650..1022
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                                                                                                                                                                                 ribonucleotide reductase
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    Hunt, T. and Standart, N.
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Kaguni, L.S.
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Best Local Similarity 77.6%;
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260 c
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Atlantic surf clam.
Spisula solidissima
Eukaryotae; mitochondrial eukaryotes; Metazoa; Mollusca; Bivalvia;
Heteroconchia; Veneroida; Mactridae; Spisula.
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                                                                                                                                                                                                                                              1507 CAAACATCATTCATAGAAAGCATATTACATACATGTTTATACATAAGCATTACATTTTT 1448
                                                                                                                                                                          1447 TAATAAAATGTATACAGGTGGGGCACTGTTTTGGTGGAAGGCTTGGAGTTTTTTAATG 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                                                                                                               71 nnvgaakthyythtnvsgadsktvtdsynasgtsssnggtdgnr-sgadsygssktamts 129
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                                                                                                                                                                                                                    130 rnrtgktannavdsrnmgdasvgsdkntkkhakns-adgkvgsknngdrnnrygtgtksn 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 mssssvvsrtascndkakkdgnttsswttdccnrtwgvcdtdttyrvnndsghnkyssan 65
                                            11 vvsrtascndkakkdgnttsswttdccnrtwgvcdtdttyrvnndsghnkyssanynygg 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 ACCGGGGCAGGCCGTGCCGGCTGAGGAGGTCCTG-AGGCTACAGAGCTGCCGCGCGCTGGC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-1992
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       2; Gaps
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S.solidissima mRNA for M2 (small) subunit of ribonucleotide
reductase.
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atches 95; Indels
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  75; Mismatches 83; Indels
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Pred. No. 3.22e-
88; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           128278 215 bp DNA
Sequence 5 from patent US 5569830.
128278
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/organism-"unknown"
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Local Similarity 11.5%;
hes 24; Conservative
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  Conservative
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FEATURES

BASE COUNT

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DEFINITION

RESULT

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KEYWORDS

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Gaps

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/product="fibroin light-chain"
/db_xref="PID:g289363"
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/db_xref="PID:g289363"
/dene="Fib-L"
/gene="Fib-L"
                                                                                                                              Eukaryouse; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Lepidoptera; Bombycoldea; Bombycdae; Bombyc. 1 (bases 1 to 14626) Kkuchi.Y., Mori.K., Suzuki,S., Yamaguchi.K. and Mizuno.S. Structure of the Bombyx mori fibroin light-chain-encoding gene: upstream sequence elements common to the light and heavy chain gene 110, 151-158 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(1069..1104,9250..9332,10532..10727,11412..11555,
12196..1284,13361..13505,14061..14156)
gene="Fib-L"
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[2196..12284,13361..13505,14061..14499)
gene="Fib-L"
                      07-MAY-1993
                                                                                      fibroin light chain.
Bombyx mori 5th instar larvae posterior silk gland DNA.
Bombyx mori
           BMOFLCEG 14626 bp DNA INV 07
Bombyx mori fibroin light-chain gene, complete cds.
M76430
                                                                                                                                                                                                                                                                                                                                                        /dev_stage="5th instar larvae"
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                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         900.907
997.1003
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2491..511
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Pred. No. 1.42e-02;
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1706..2043
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131 c 74 g 2125 t
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GAIGGLONGYSLRKLMAPSSINHIGWMISSLMISSSIWLIPFFFYSFSYVLTFWNIF
KLFHLNOLESWFVNSKIIKFTLEMNFLSLGGLPPFUGFLEKWIVYQOLTIKNOYPMLT
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Ballard, W., Olsen, G.J., Faith, D.P., Odgers, W.A., Rowell, D.M. and Atkinson, P.W.
Evidence from 12s ribosomal RNA sequences that onychophorans are
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Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Direct Submission
Submitted (03-0CT-1995) Laurie S. Kaguni, Blochemistry Department,
Michigan State University, East Lansing, MI 48824-1319, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences; sequence is a composite containing sequences obtained from different Drosophila melanogaster strains"
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                                                                                                                        Satta,Y. and Takahata,N. Evolution of Drosophila mitochondrial DNA and the history of melanogaster subgroup
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/note="Description: mitochondrial NADH-ubiquinone oxidoreductase chain 6"
/db.xref="Flybase:FBgn0013685"
/product="tRNA-f-met (CAU)"
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/mitochondrion
/note="derived from new and previously submitted
                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9558-9562 (1990)
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      Drosophila melanogaster and its sibling species
Mol. Biol. Evol. 4 (6), 638-650 (1987)
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171..239
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Science 258 (5086), 1345-1348 (1992)
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Genetics 118 (4), 649-663 (1988)
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                                    Mol. Biol
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Transfer RNA genes in Drosophila mitochondrial DNA: related 5'
flanking sequences and comparisons to mammalian mitochondrial tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A-T-rich region; ArPase; circular; complete genome; cytochrome b; cytochrome c; cytochrome c oxidase; mitochondrial DNA; NADH dehydrogenase; ribosomal RNA; transfer RNA-Ala; transfer RNA-Arg; transfer RNA-Arg; transfer RNA-Arg; transfer RNA-Gln; transfer RNA-Glu; transfer RNA-Glu; transfer RNA-His; transfer RNA-His; transfer RNA-His; transfer RNA-Flu; transfer RNA-Flu; transfer RNA-Ser; transfer RNA-Flu; 
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Mitochondrion brosophila melanogaster
Eukaryotae; mitochondrial eukaryotes: Metazoa; Arthropoda;
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.

[ (bases 1 to 408; 13319 to 19517)

Lewis, D. L., Farr, C. L. and Kaguni, L. S.
Drosophila melanogaster mitochondrial DNA: completion of the nucleotide sequence and evolutionary comparisons

Insect Mol. Biol. 4 (4), 263-278 (1995)
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Drosophila melanogaster mitochondrial genome, complete sequence.
U37541
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Satta,Y., Ishiwa,H. and Chigusa,S.I.
Analysis of nucleotide substitutions of mitochondrial DNAs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Molstenholme, D.R.

Drosophila michochondrial DNA: a novel gene order

Nucleic Acids Res. 10 (21), 6619-6637 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 35;
Pred. No. 1.42e-02;
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                                                            /number=6
14061..14499
/gene="Fib-L"
                                                                                                                                                                              14473..14478
/gene="Fib-L"
14499
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de Bruijn, M.H.
13506..14060
/gene="Fib-L"
                                                                                                                                                                                                                                                                               /gene="Fib-L"
2726 c 2
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Best Local Similarity 70.0%;
Matches 63; Conservative
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NNNSNNTSSNSKNNNIKETIELGGHOGSIEKISWSPKNNDLLASAGTDKVIKIWDVK
IGKCIGTVSTNSENIDVRWSPOGQEIVACTRDBHALIDLPTKTLKTYKRNGEELNO
VGWDNNGDLILMANSWGHIRAYKFRESTFRCTRYKHLKTYGHTASIYCMEPDPTGKYLA
AGSADSIVSLWDIEDDMCVKRFIKSTFRCTRSVSFSFDGOFIAASSFESTIEIFHIESS
OPIHTIECSGVSSLAWHPTLPLLAYAPEINENNKDPSIRVEGYHS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="PGGFQHLQQQQQQQQQQQQQQQQQQQQQQQQQQQUQQHQQHNQ
QIQQQAQATQQHLQTQQYLQSQIHQQSQQSQLSNNLNSNSKESTNIPKTNTQYTNFDS
KNLDLASRYFSECSTKDFIGNKKKSTSVAWNANGTKIASSGSDGIVRVWNFDPLGNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1427)
Shaw,D.R., Richter,H., Giorda,R., Ohmachi,T. and Ennis,H.L.
Shaw,D.R., Richter,H., Giorda,R., Ohmachi,T. and Ennis,H.L.
Nuclectide sequences of Dictyostellum discoideum developmentally
regulated cobhs rich in (AAC) imply proteins that contain clusters
of asparagine, glutamine, or threonine
Mol. Gen. Genet. 218 (3), 453-459 (1989)
                                                                                                                                                                                                                                                                                                                                                                               1500 CAT-TCATAGAAAGCATATTACATACATGTTTATACATAAGCATTACATTTTTTAATAA 1442
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                                      /db.xref="FlyBase: BBn0013685"
/product="tRNA-Asp (GUC)"
3907..4068
/pcne="mt:Nb6"
/note="Description: mitochondrial NADH-ubiquinone oxidoreductase chain 6"
/note="Description: mitochondrial NADH-ubiguinone
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                                                                                                                                                                                                                                                                             Length 19517;
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Pred. No. 1.42e-02;
0; Mismatches 41; Indels
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/clone_lib="lambda gil0"
/clone="AAC3"
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/db_xref="PID:97176"
/db_xref="SWISS-PROT:P14197"
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198 c 200 g 431
                           oxidoreductase chain 6"
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Dictyostelium discoideum
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2.0%;
Best Local Similarity 65.0%;
Matches 78; Conservative
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Best Local Similarity 78.8%;
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/traini_table=5
/traini_table=5
/traini_table=5
Ligddolynvivalafyllefynefhiggegnwivplakigaddmapprannysfyl
Ligddolynvivalafyllefynefhiggegnwivplakigaddmapprannysfyl
Ligddolynvivalafyllefylefyllefyldefyldalissilgav
Neityvivalnysfgegnylivplakiefyryvivillefyldyndalimysfyl
Dpagggdplivyuplefypryiillefgegnishiiggesgkefyrdiyami
Aigligfylwahhhefygaddynfaryfyathiavpfgikifsmiatlhgfolsysp
Ailwalgfyldgictovllanssvoliilhfyrvyahhefyldyngaryfymi
WYPLFTGILLNWKKSHFIIMFIGVNLTFFPOHFLGLAGMAPRIYSDFDAGFTI
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LIFFNNYNRFLLHGQLIEBHWTILIFATILLFFAFSALLLYLTDETHESPYTLKGTGH
GWYWSYEYSDFWINTEDSYMIFNELMTDGFRLLDVDMRVVLPMNSQIRILVYAADVI
HSWTVPALGVKVDGTPGRLNQTNFFINRPGLFYGQCSEICGANHSPMPIVLESPUVIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxidoreductase chain 6; ATAA, putative translation infilation codon for cytochrome c oxidase subunit Ir /db_xref="Flybase:Fbgn0013685" <1474.3009
                                                                                                                                                                                                                                                                                                                                                                       /note="pescription: mitochondrial NADH-ubiquinone oxidoreductase chain 6" /db_xref="FlyBase:FBgn0013685"
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/note="Description: mitochondrial NADH-ubiquinone oxidoreductase chain 6"
/codon_start=1
/db_xref="Flyamse: Flyamse: Flyamse: Flyamse: Flyamse: Flyamse: Flyamse: Coxidase subunit I"
/db_xref="Pib:g1166531"
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/note="Description: mitochondrial NADH-ubiquinone
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                                                                    /note-"Description: mitochondrial NADH-ubiquinone
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/product="cytochrome c oxidase subunit II"
/db_xref="PID:g1166532"
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/product="tRNA-Leu (UAA)"
3083..>3767
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3840..3906
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complement(1403..1468)
                                                                                                               /db_xref="FlyBase:FBgn0013685"
/product="tRNA-Trp (UCA)"
complement(1322..1383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"tRMA-Tyr (GUA)"
1470..1473
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DEFINITION ACCESSION

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KEYWORDS SOURCE

AUTHORS TITLE

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AUTHORS

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MTNF1VTPOQTQGHCAENPEGGICQDDSGCTPGKAERKAQGIRTGNCVPFNGTVKTCE
ITGGCPVEVDDKIPSPALLREAENFTLFIKRSISPPRFWNRALVPESWGTYMKRCL
YHKIQHPLCPVFNLGSYVPRESGODFFSLAEKGGVVGITIDWRCDLDMHVHCKPIYQF
HGIYTGEKNLSPGFNTRFRARHEYQNGTNRRHLEKVFGIHFDILVDGKRAGKEDIIPTHTT
IGSGIGIFGVATVLCDLLLLHILPKRHYYKQKKFKYAEDMGPGEGEHDPVATSSTLGL
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/db_xref=n=n=0;
/translation=MARRLQDBLSAFFEYDTPRMYLVRNKKVGVIFRLIQLVYLVYV
IGWVFVYEKGYQTSSDLISSVSVKLKGLAVTQLQGLGPQVMDVADYVFPAHGDSSFVV
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                                                                                                                                                                                        Murinae; Rattus.

"I (bases 1 to 1837)
Valera, S. Hussy, N., Evans, R.J., Adami, N., North, R.A.,
Surprenant, A. and Buell, G.
An ew class of 11gand-gated ion channel defined by P2x receptor for extracellular ATP
Nature 371 (6497), 516-519 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Direct Submission
Submitted (21-JUL-1994) G.N. Buell, Glaxo Inst of Mol Biology, 14
Chemin des Aulx, 1228 Plan-les-Ouates, Geneva, SWITZERLAND
Location/Qualifiers
                                                                                                       Norway rat.
Ratus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1862)
Millward-Sadler,S.J., Hall,J., Black,G.W., Hazlewood,G.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Fungi; Chytridiomycota; Chytridiomycetes; Neocallimasticaceae;
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/organism="Rattus norvegicus"
/cell_type='smooth muscle"
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Piromyces sp. mRNA for endo-bl,4-mannanase.
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Piromyces sp.
Piromyces sp.
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R.norvegicus P2X mRNA.
X80477
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Best Local Similarity 72.3%;
Matches 47; Conservative
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Gilbert, H.J.
Direct Submission
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ATP receptor; P2X
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NSAVTLGPRRVEJAPLDSPESSESSENHUMBRYLLEDERYSYNEVPDYHEDHITYL
REMEYKCKRVVSTRKQPPINSMRAILVDWLVPGEEXKLONFTHLANNY IDRELS
SMSVLRGKLQLVGTAAMLLASKPEEIYPPEVAEFVYIIDDTYTKKOVLRHEHLVLKVL
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HLALYTVTGQSWPESLVQKTGYTLETLKPCLLDLHQTYLRAPQHAQQSIREKYKNSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In the 'Structure' publication: The 5'end of clone A3 was made by PCR, and introduced a methionine in place of a valine, followed by a glycine to make an NooI site. At the 3' end, an XhoI site was engineered in to allow subcloning into pET2Id, which also puts 6 histidines at the C-terminus that were used for purification. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     cobayashi, H., Stewart, E., Poon, R., Adamczewski, J.P., Gannon, J. and
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                                                                                                                                                       Vertebrata; untochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos. 1 (bases 1 to 1512)
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The crystal structure of cyclin A
Structure 3 (11), 1235-1247 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="subunit structure-cyclin A /p34cdc2 or cyclin A /p33cdk2"
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                                                                                                                                                                                                                                                                                                                     Submitted (08-SEP-1992) T. Hunt, ICRF Clare Hall Laboratories, South Mimms, Herts EN6 3LD, UK
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Pred. No. 1.59e-01;
0; Mismatches 18; Indels
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                                                                                                                      cyclin A; protein kinase activation. domestic cattle or domestic cow.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"Cyclin A-3"
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                         B.taurus mRNA for cyclin A. X68321
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Matches 47; Conservative
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source

FEATURES

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TITLE JOURNAL MEDLINE COMMENT

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AUTHORS

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14

RESULT

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BASE COUNT ORIGIN

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Gilbert, H.J.

Evidence that the Piromyces gene family encoding endo-1.4-mannanases arose through gene duplication FEMS Microbiol. Lett. 241, 183-188 (1996)

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          1..1862
/organism="Piromyces sp."
1..1710
/gene="manc"
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355 9 229 c 651 BASE COUNT ORIGIN Query Match 1.9%; Score 30; DB 64; Length 1862; Best Local Similarity 69.7%; Pred. No. 4.81e-02; Matches 62; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

셤 ò 1834 taaataanaaataaaaaaaaaaa 1862

1534 TATGGGAGAACCAAAAAAAAAAAAAAAA 1562 g ô

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

Thu Nov 6 10:11:33 1997; MasPar time 169.52 Seconds 962.304 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-842-827-1 (1-1563) from US08842827.seq 1563 Title:

Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

142080 segs, 52183452 bases x 2 Dbase 0; Query 0 ٠. STD Searched: Nmatch

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq28 lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28

Mean 9.613; Variance 6.601; scale 1.456 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Sc 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Score	Query					
)	Match	Match Length DB	BB	ID	Description	Pred. No.
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ın v	45	2.9	204	Н	N81164	Base substituted E.co	8.06e-10
4	41	2.6	91	φ	051746	Oligonucleotide probe	8.33e-08
פ	38	2.4	204	Н	N81164	Base substituted E.co	2.50e-06
7	36	2.3	114	12	070468	Generic DNA sequence	2.32e-05
ص ص	36	2.3	114	12	070467	Generic DNA sequence	2.32e-05
٥ 0	34	2.5	67	74	T14322		2.07e-04
10	32	2.5	114	12	070469	Generic DNA sequence	6.95e-05
11	34	2.2	114	12	070465	Generic DNA sequence	2.07e-04
12	34	2.5	114	12	070467	Generic DNA sequence	2.07e-04
c 13	35	2.2	114	12	970465	Generic DNA sequence	6.95e-05
c 14	34	2.5	114	12	070470	Generic DNA sequence	2.07e-04
c 15	34	2.2	114	12	070468	Generic DNA segmence	2.070-04

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ALIGNMENTS

00-APR-1991 (first entry)
Muman Natriuretic Peptide Receptor B.
NPRB: ANP: BNP: CNP: kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase. /label- extracellular domain /note- "binds natriuretic peptides A,B and C]" Domain 456.456 /label- transmembrane domain 479..1047 /label cytoplasmic domain /note "GC and protien kinase activity" Modified site 24..26 /label Nglycos_site Modified site 35..37 /label Nglycos_site Modified site 161..163 /label Nglycos_site Modified site 161..163 Location/Qualifiers JT 1 Q10572 standard; DNA; 1047 BP. /label N-glycos_site
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Modified -site 600..602
WOSD_0029.A.
10-JAN-1991. /label signal sequence Protein 12 23..455 /label- mature NPBR Homo sapiens Peptide Domain DOS NAME OF THE PROPERTY OF TH

US-08-842-827-1.rng

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278 rtrnnananznanntvnvntyrnnnnnngnnnnnnnnrarndngvnngnsnmnnnagen 337
         National Control of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr—144,952). The protein of the control of the contro
                                                                                                                                                                                                                                                                                                            09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB: ANP: BNP: CNP: kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "binds natriuretic peptides A,B and C]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //abel- cytoplasmic domain
/Aoote- "GC and protien kinase activity"
Modified -site 24..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 C;
                                                                                          949 rnhdnnrnrngvhtgnvcagvvgnkmnr 976
                                                                                                                                                403 CCAGCCAGCAACACGCAGAGCACATCGA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
                                                                                                                                                                                                                                                         010572 standard; DNA; 1047 BP. Q10572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1990; U03586.
23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe D;
WPI; 91-03671L/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tabel transmembrane domain 479..1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain 23..455
/label- extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label N-glycos_site
Modified -site 35.37
/label N-glycos_site
Modified -site 161.163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- N-glycos_site
Modified -site 244..246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabel N-glycos site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label = N-glycos_site
4odified -site 349..351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide 1..22
/label- signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label N-glycos_site
Modified -site 277..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1047 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .059 TTGCAACCAGAGCTCCCTGAATGAGTCCAGTCAACACATCGCTCCAGTGGTGTTTATAAT 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 yndartddrnhyntnngvnnanngsnnsvnhnvyarnnggnnnathnnrangrnvyncgn 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 nnmnhnnnnanrnnntngdyvnnyndvngnsnragntratgrnwndnrtrnnananna 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 nntvnvntyrnnnnnnnynnnnrnnnrarndngvnngnsnmnnagcnydgnnnyanvnn 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761 TITIGACCAATCIGGAICACAACAICCAAGAAGIGAGGCCGCAGICIGCCIAIIGAAIA 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643
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                                                                                                                                                         National July 1992.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 9.0%; Pred. No. 4.56e-27; les 73; Conservative 213; Mismatches 517; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 77; DB 2; L/9.0%; Pred. No. 4.56e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 A;
                                                                                    Chang M, Goeddel D, Lowe D; WPI; 91-036711/05.
22-JUN-1990; U03586.
23-JUN-1989; US-370673.
                                                      (GETH ) GENENTECH INC
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4.7%; Score 74; DB 2; Length 1047; larity 7.9%; Pred. No. 2.16e-25; Conservative 215; Mismatches 479; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 GTATIATCGTTATTATTCTTGGAGAAACCCTGTCTGTTTACTGTAACCTTTTGCACTCAA 600
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                                                                                                               54 GAGGTCTGAGGCTACAGAGCTGCCGCGGCTACGAGAGGCGCCTCGGCACTAACCGAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 ACTICAAGGCATACCCCCTTCCAACGAG-GAGTATTCTGTAATGATGAGTCCATCAAGTA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           snrgssygsnmtahgkynnnantghnkgnvvankhvnkkrnnntrnvnnnnkhmrdvnnn 577
                                                                 338 ydgnnnyanvnnntnnnggtrndgnrnvnkmngrryhgvtgnvvmdknndrntdnvnwam 397
                                                                                                                                                                                                           398 gåndsgdnnnaahysganknnwwtgrnnnwvkgannsdnnncandnddnscdktnnstna 457
4 GTGGGAGAGAGCGCCGGGATCCGGACGGGGTAGCAACCGGGGCCAGGCCGTGCCGGGTGAG 63
                                                                                                                                                                                                                                                            601 ATTCCTTTATCAGGAATAACTACATAGCCACTATTTACAAAGCCATTGGAACCTTT-TA
                                                                                                                                                                                                                                                                                                                                                    458 nvangtgotonmngvssonnorknmonknoasmnwrorwnonnognsoryhkgagsroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 GGCGGTCGCCAGCCCCGGCCCGGGCTCGATAATCAAGGGCCTCGGCCGTCGTCGTCCCGCACC
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Oligomoticotides probe MK14-A consists of nucleotides 5-95 of MK14 (0519735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may
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051746;
31-MAY-1994 (first entry)
01igonucleotide probe MK14-A
01igonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligo:nucleotide probes specific for Mycobacteria – used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          997 nknhvssttkdandnngcnnnnrgdvnmkgkgkmrtyw 1035
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01-DEC-1993: 108325.
24-MAY-1993: 05-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD. Spears PA; WPI; 93-378844/48.
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SUSO) STOWEN SOKERIOY.

11 Lehtovacra P, Knowles J, Koivula A, Bamford J, Reinikainen T;
Lehtovacra P, Knowles J, Koivula A, Bamford J, Reinikainen T;
RMF1: 88-279927/40.

12 Introducing random point mutations into nucleic acods -
Throughous stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.

12 misincorporation, completion of molecules and screening.

13 Sandom point mutations were introduced into the alpha fragment of
15 Random point mutations were introduced into the alpha fragment of
15 Random point mutations were introduced into the alpha fragment of
16 E-coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to
16 operate a popn of DNA molecules which terminate at all
17 possible nucleotide positions within a specified region. The
18 variable 3' ends generated in this way are used as primers for
18 reverse transcriptase. Nucleotides are misincorporated by the
18 remscriptase and the molecules are completed to forms that can be
18 maplified and then expressed in a suitable host-vector system.
18 C The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynv 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                            Gaps
                                                                                                                                                                  61
                                                                                                                                                                                                                                                                  N81164;
08.NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 Others;
                                                                                                                                          5 ccggcgssvhsyyvvhvvshhhsvhhvhvhvhvvhvvhhvhhvhyhvyvsvc
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
De useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 204;
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                                                                                                          Indels
                                                                     91;
                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 C; 17 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 hnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhc 186
                                                                                      Pred. No. 8.06e-10;
46; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 1; L. Pred. No. 8.06e-10;
                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            occurred singularly in any given mutant. See also P80575.
                                                                       Score 45;
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /*tag- a
/function=multiple cloning site
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                                                                                                                                                                                                                                             N81164 standard; DNA; 204 BP.
                                                                     2.9%;
8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.9%;
Best Local Similarity 12.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q51746 standard; cDNA; 91
Q51746;
                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-APR-1987; US-034819.
                                                                                                                                                                                                                                                                                                                                                                              19. 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1988; 105163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 BP;
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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EP-571911-A.
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                                                                       Query Match
                                                                                          Best Loca
Matches
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SUSO) SUGNEW SOKERA OY.

Lichtovaera P., Knowles J., Koivula A., Bamford J., Reinikainen T;
Lehtovaera P., Knowles J., Koivula A., Bamford J., Reinikainen T;
Lehtovaera P., Knowles J., Koivula A., Bamford J., Reinikainen T;
Introducing random point mutations into nucleic acods -
Thy prepr of single stranded template, annealing a primer, elongation,
PT misincorporation, completion of molecules and screening.

PS Random point mutations were introduced into the alpha fragment of
E. Coil beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonuclectide was hybridised to
E. Coil beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonuclectide was hybridised to
E. Coil beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonuclectide was hybridised to
E. Coil beta-galactosidase. Nucleotides with terminate at all possible nucleotide positions within a specified region. The reverse transcriptuse. Nucleotides are misincorporated by the transcriptuse and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                               7 ggcgssvhsyyv-vhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhvhvvsvctcaa 65
                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 T; 108 Others;
                                                                                                                                                                 Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of 1 (Q5135). It hybridized to all spp. of mycobacteria tested, 1 cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                              New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 204;
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Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                               Length 91;
                                                                                                                                                                                                                                                                                                                             Score 41; DB 9; Le
Pred. No. 8.33e-08;
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                                                                                                                                                                                                                                                                                                                                                                   47; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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63; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function-multiple cloning site
orimer_bind 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA; 204 BP
                                                        (BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            larity 19.5%;
Conservative
                                                                                                                                                                                                                                                                                                                             Query Match 2.6%;
Best Local Similarity 10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 A;
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                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
                24-MAY-1993; 108325.
26-MAY-1992; US-889651
                                                                          Shank DD, Spears PA;
WPI; 93-378844/48.
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les 31; Conser
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PT Generifying proceins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or pertaining a recombinant vector library expressing fusion proteins comprising a blading domain and an effector domain promprising a blading domain and an effector domain prospecial and blading domain and an effector domain processories and processories as follows: X(NNB) LITGC)(NNB) 62(NNB) 7(TGC)(NNB) 10%. X and X are flanking restriction sites (X is not the same as Y) that are not processoried further. Other generic sequences are shown in 700466-68. Other specific peptides generated by these generic sequences are shown in 700466-68. Other specific peptides generated by these generic sequences are shown in 700466-68. Other specific peptides generated by these generic sequences are shown in 70046-68. Other specific peptides generated by these generic sequences are shown in 70046-68. Other specific between the 2 domains The Japanous or peptides portion that is chemically or biologically active. They may further comprise a linker appealed between the 2 domains. The oliver of contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eq. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the concolonal or polyclonal antibodies and therefore circumvent the need for concolonal or polyclonal antibodies and therefore circumvent the need for compens methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
Generic DNA sequence to generate a random TSAR petide library.
TSAR, totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment, generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.32e-05;
34; Mismatches 74; Indels
                                                                                     181 GGCGCTCCCACCGCCAGCAATGGCGCCCGGGGGCCTCCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                       can be
                                                           154 ccbnahvchavhbnahrnwayvrhdarrddvhccvchcc
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ',2,
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "this sequence represents 'Z'; Z sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
55..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-125...
30-DEC-1993; US-17550...
31-DAN-1994; US-189331.
(UNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                      070468 standard; DNA; 114 BP.
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P-PSDB; R65154.
                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9418318-A.
                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comments >
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                                                                                                                                                                     RESULT
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bgcaggycgacbcyrraggnyccccggggywccgagcycgaayycdchvgccgymrttthh 93

34 Matches

8

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fingerprinting
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                            misc_feature
                                                                                                                 13-OCT-1994;
                                                                                                                                9-DEC-1994;
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                                                                                        25-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comments)"
 Synthetic.
                                                                                                                                                                 Brenner S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPT referring proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins by a binding domain and an effector domain can also be represented as follows: X(NNB) EG(NNB)12(NNB)16(TGC)(NNB)17. X ond Y are flanking restriction sites (X is not the same as Y) that are not specific peptides generated by these generic sequences are shown in Graffic peptides generated by these generic sequences are shown in Graffic peptides generated by these generic sequences are shown in Graffic peptides generated by these generic sequences are shown in Graffically for a ligand and second effector peptide portion that is chemically or biologically active They may further comprise a linker peptide between the 2 domains: The Oligomicleotides are also designed confer some degree of conformational rigidity to the peptides. These residues confer some degree of conformational rigidity to the peptides. They are active for confer some degree of conformational rigidity to the peptides. They can conformation of maching to the specific target or on the readlostope, peptide, toxin or enzyme, to the specific target or on the complex methods of hybridoma formation of macromolecules, eg. The Arrest and rapid defection in vivo antibody production.

The SARS are easily characterised and therefore circumvent the need for the real are easily characterised and therefore circumvent the need for the real are easily characterised and therefore circumvent the need for the real are and rapid defection in vivo antibody production.
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                                                                   Generic DNA sequence to generate a random TSAR petide library.
TSAR, totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 CCCTCACAGCCCCGGGGACACTCGGTTAGTGCCGAGGGGGTTCGTGTGCCAGCCGGGGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-1997 (first entry) Primer used in the labelling and sorting of nucleotide molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 GCTCTGTAGCCTCAGGACCTCCTCAGCCGGCACGCCTGCCCCGGTTGCTAC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 12; Length 114;
Pred. No. 2.32e-05;
32; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Labelling; sorting; sequencing; tag; tagging; ss.
                                                                                                                                                                                        /note= "this sequence represents 'Z'; Z can be a sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                            Location/Qualifiers
55..60
         JT 8
O70467 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                           01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T14322 standard; DNA; 67 BP T14322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3%;
Similarity 5.4%;
6; Conservative
                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                        Fowlkes DM, Kay BK;
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Best Local Similarity
Matches 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R65153
                                                                                                                                                                                                                                                18-AUG-1994.
01-FEB-1994;
                                                                                                                                                                         /*tag- a
/note- "this
                                                    05-APR-1995
                                                                                                                                                           misc_feature
                                                                                                                                Synthetic
                                                                                                                                                                                                                        comments)
                                        970467;
            RESULT
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25582
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07-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                             - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hingerprinting bis consistent of a target polynucleotide Disclosure; Page 19; 71pp; English.

Determining the nucleotide sequence (I) of a target polynucleotide CT) comprises: (a) generating from T a plurality of fragments that cover T; (b) attaching an oligonucleotide tag from a repertoire of tags, to each fragment such that all the same fragments have the same tag, and all different fragments have different tags; (c) sorting the fragments by specifically hybridising the tags with their respective tag complements; (d) determining (I) of a portion of each of the fragments; and (e) determining (I) of T by collating the sequences of the fragments. The tagging system can be used with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the sequences of the framments. The tagging system can be used with single base sequencing methods to sequence polynucleotides up to single base sequencing methods to sequence polynucleotides up to thousands of fragments of a target polynucleotide to be sorted onto one or more solid phase supports and sequenced simultaneously. This sequence represents a primer which could be used to reverse transcribe mRNA. If the amplified product is then needed to be attached to a solid phase support a sequence like the one given in 11423 may be used. The mRNA would then be removed and the second strand of CDNA produced using a primer with a similar form to that described in T14324. After restriction enzyme digestion, the conjugate would have the formula described in T14325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 96-222023/22.
Labelling and sorting mols. using oligo:nucleotide tags - use
large-scale parallel operations, e.g. DNA sequencing and mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 94-279739/34.
Identifying proteins or peptide(s) which bind a ligand - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 24; Length 67;
Pred. No. 2.07e-04;
23; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ø
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/note* "this sequence represents '2'; 2 can be
sequence of 6,9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 6;
Location/Qualifiers
67
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55..60
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                                                                                                                                                                                                                                                                                                                                (LYNX-) LYNX THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q70469 standard; DNA; 114 BP
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(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, RAY BK;
                                                                                                             /mod_base= Linked to biotin w09612039-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Conservative
                                                                                                                                                                                                                                                          US-322348.
US-359295.
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US-176500.
                                                                                                                                                                                                                          12-OCT-1995; U12678
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                                                                                                                                                                                                                                                                                                                                                                                  2 genabanbanbanbanbanbanbanbanbanbtgenabanbanbanbanbanbannanna 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generic DNA sequence to generate a random TSAR petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                           Gaps
 expressing fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                         209 TCTCCTCCTCCGCTGGGAGGGGCCGTATCTCGGGGGCCGTCGCCAGCCCGGC 261
                                                                                                                                                                                                                                                                                                                    DB 12; Length 114;
                                                                                                                                                                                                                                                                                                                                       74; Indels
          comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English.
                                                                                                                                                                                                                                                                                             4. T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "this sequence represents '2'; 2 can be a sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                            Pred. No. 6.95e-05;
                                                                                                                                                                                                                                                                                                                                        31; Mismatches
                                                                                                                                                                                                                                                                                             4
G;
 screening a recombinant vector library
                                                                                                                                                                                                                                                                                                                    Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                             4
C,
                                                                                                                                                                                                                                                                                detection in a screening process.
Sequence 114 BP: 0 A: 4 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q70465 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                  2.28;
                                                                                                                                                                                                                                                                                                                            Larity 7.1%;
Conservative
                                                                                                                                                                                                                                                                                             0 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R65150 and R65151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-013416.
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                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comments)"
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      070465;
                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in 070466-68.

Other specific peptides generated by these generic sequences are shown in 86511-54. Takes are concatenated by these generic sequences are shown in affailty for a ligand and a second effector peptide portion that is affailty for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 eysteine residues positioned in, or flanking, the unpredicted or variant residues positioned confer some degree of conformational rigidity to the peptides. The TSARs or compens. Comprise comprision a TSAR binding domain can be used in vivo to radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. metal ion, proclonal antibodies and therefore circumvent the need for complex methods of hybridoms formation or in vivo antibody production. The TSARs are easily characterised and have designed and each the section of a second conduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins occuprising a binding domain and an effector domain bisclosure. Page 35, 255pp; English.

010467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X (NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in 070466-68.

Other specific peptides generated by these generic sequences are shown in R55151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is elemically or biologically active. They may further comprise a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 GCCTCGGCACTAACCGAGTGTTCGCGGGGGCTGTGAGGGGAGGGCCCCGGGCGCCCATTGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 bandandandandandtgcandandandandandandandandandandandandan 62
                                                                                                                                                                                                                                                                                                                                                                                                             activity allowing direct control of 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.07e-04;
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/note* "this sequence represents 'z'; z can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 55..60
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30-DEC-1993; US-176500.
31-DAN-1994; US-189331.
(UVNC-) UNIV NORTH CAROLINA.
FOWIXES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%;
Similarity 3.6%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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eg. + the need

screening process

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peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or compans, comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or necessity complex methods of hybridomal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
                                                                                                                                                                                                                                                                                                                                         direct and rapid detection in a screening process Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
         8888888888888888
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ö Gaps ö Score 34; DB 12; Length 114; Pred. No. 2.07e-04; 33; Mismatches 71; Indels 2.2%; s. larity 1.9%; F. Conservative 3 Local Similarity Query Match Matches

121 GAGTGTTCGCGGGGGCTGTGAGGGGAGGGCCCCGGGGCCCATTGCTGGCGGTGGGAGCGC 180

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181 CGCCCGGTCTCAGCCCGCCTCGGCTGCTCTCCTCCTCCGGCTGGG 226 à

French Rossian (1921) and the following a recombinant vector library expressing fusion proteins recenting a recombinant vector library expressing fusion proteins are compliant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins. PS comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English STILS generic formula can also be comprehent Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB) GTGC) (NNB)112(NNB)14(TGC) (NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not x specific peptides generated by these generic sequences are shown in CC comprising at least two functional regions - a binding domain with a finity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with a finity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of peptide between the 2 domains. The oilgonuclectides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues residues positioned in, or flanking, the unpredicted or variant residues. There residues confers some degree of conformational rigidity to the peptides. The TSARS or comprising a TSAR binding domain can be used in vivo to deliver a chemically or bloogically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the Generic DNA sequence to generate a random TSAR petide library.
TSAR, totally synthetic affinity reagent, synthetic, binding donain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss. /*tag- a /note- "this sequence represents 'Z'; Z can be a sequence of 6, 9 or 12 nucleotides (see Location/Qualifiers 30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
UWNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
WPI; 94-279739/34.
P-PSDB; R65150 and R65151. 070465 standard; DNA; 114 BP. (first entry) US-013416 55..60 000977 18-AUG-1994. 01-FEB-1994; 05-APR-1995 misc_feature 01-FEB-1993; Synthetic.

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Gaps

Length 114;

Score 34; DB 12; Length 114 Pred. No. 2.07e-04; 29; Mismatches 72; Indels

2.2%; 9.8%;

Query Match Best Local Similarity

11; Conservative

Matches

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referritying proteins or peptide(s) which bind a ligand - by
referritying proteins or peptide(s) which bind a ligand - by
screening a recombinant vector library expressing fusion proteins
comprising a binding domain and an effector domain
bisclosure; Page 36; 25pp; English.

CO0470 is a generic DNA sequence used to generate random TSAR (Totally
synthetic Affinity Reagents) peptides; This generic formula can also be
spresented as follows: K(NNB)4(CAC)(NNB)8(CAC)(NNB)8

CCC (CAC)2(NNB)Y. X and Y are flanking restriction sites (X is not the same
as Y) that are not specified further. The peptides generated by this and
other generic sequences (7074173) have invariant histidine residues
incorporated into variant sequences. TSARs are concatenated
beterofunctional proteins or peptides, comprising at least two functional
regions - a binding domain with affinity for a ligand and a second
effector peptide portion that is chemically or biologically active. They
may further comprise a linker peptide between the 2 domains. The TSARs
or compans. comprising a TSAR binding domain can be used in vivo to
deliver a chemically or biologically active molety, eg. metal ion,
cradioisotope, peptide, toxin or enzyme, to the specific target or on the
monoloual or polytopal antibodies and therefore circumvent the need
                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening proce
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/note= "encoded by Z (see comments)"
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similarity 3.7%;
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US-176500.
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P-PSDB; R58378.
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Generic DNA sequence to generate a random TSAR petide library.
TSAR: totally synthetic affinity resegent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                     90 GCGCAGCTCTGTAGCCTCAGGACCTCCTCAGCCGGCACGGCCTGCCCGGT 39
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O70468; standard; DNA; 114 BP.

O70468; tandard; DNA; 114 BP.

DT 05-APR-1995 (first entry)

DE Generic DNA sequence to generate

NW firect; rapid; detection; screen

OS Synthetic.

FT Atgs a

FT Atgs a

FT Comments)

NO418318-A.

PP 01-FEB-1994; U00977.

PR 01-FEB-1994; US-18931.

PR 01-FEB-1994; UNAV NOTH CAROLINA.

PR 01-FEB-1994; US-18931.

PR 01-FEB-1994; US-18931.

PR 01-FEB-1994; US-18931.

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                                                                                       Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

Result

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                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Fins clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 600 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 478.
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Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/lab_host="DH10B (ampicillin resistant)"
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/sex="unknown"
                                                                                                                                                                                                                                                                                                                            Score 482; DB 28;
Pred. No. 0.00e+00;
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98.4%;
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Best Local Similarity 98.4%;
Matches 507; Conservative
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llinl.gov) for further information.
Seq primer: -28Mls revo from Amersham.
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20-NOV-1996 S2020d08.rl Stratagene colon (#937204) Homo sapiens CDNA clone 58439 5. AA133640
                                                                                                                                                                                            Eukaryotee; mitochondrial eukaryotee; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 390)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikhn, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1810
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/lab_host="SOLR cells (kanamycin resistant)"
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07-MAR-1997 (Rel. 51, Last updated, Version 2)
2b63f08.rl Soares fetal lung NDHL19W Homo sapiens CDNA clone 308295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This Clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@lange.llnl.gov) for further information. Insert Length: 773 Std Error: 0.00 Seq primer:
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Holman M., Rultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Tan F., Trevaskis E.,
Waterston R., Williamson A., Wohldmann P., Wilson R.;
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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                /organism="Homo sapiens"
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                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40Mi3 fwd from Amersham
High quality sequence stop: 285.
Location/Qualifiers
                                                                                      zo20d08.sl Stratagene colon (#937204) Homo sapiens cDNA clone
587439 3'.
AA132534
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Waterston, R., Williamson, A., Mohldmann, P. and Wilson, R., Washu-Merck Est project
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
FER: 314 286 1810
Fax: 314 286 1810
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/lab_host="SOLR cells (kanamycin resistant)"
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Pred. No. 0.00e+00;
0; Mismatches 2;
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AA062861 377 bp mRNA EST 02-FEB-1997 zf70e10.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 382314
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                                                                                                                                                                         1547 TIGETICICCCATACATITITAATATGTATITAAATATATATATATAAATCAAACATCATICATAGAAG 1488
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Hilliar, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kuchba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Washu-wack, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                       Contact: Wilson RX
Washlwherck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
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                                                                          Length 378;
                                                                        Score 352; DB 28; Length 37:
Pred. No. 0.00e+00;
0; Mismatches 1; Indels
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/organism="Homo sapiens"
complement(<1..>378)
68 c 75 g
                                                                        ch 22.5%;
1 Similarity 99.2%;
365; Conservative
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 600 Std Error: 0.00 Seq primer: -40ml3 fwd. from Amersham High quality sequence stop: 341.
                                   240
                                                                                                                                                                     241 agg-aagaggatgcatctttcttcctggtgtacaagcetttaaagacttctgctgctgct 299
                  tacaactctgcatgaaacaccaacaactgggaatcactatccgagcaatcaccagccttg 180
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Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Materston, R., Milkin, L., Rohlfing, T., Tan, F., Trevsskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                                                                                           1256 AGGCAAGAGGATGCATCTTCTTCTGGTGTACAAGCCTTTAAAGACTTCTGCTGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1810
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/sex="unknown"
/dev_stage="19 weeks"
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Matches 306; Conservative
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zf70d09.rl Soares pineal gland N3HPG Homo sapiens cDNA clone 382289
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Hiller. L., Clark.N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                        Score 345; DB 30; Length 377;
Pred. No. 0.00e+00;
0; Mismatches 1; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
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1 Similarity 99.2%;
358; Conservative
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Best Local Similarity
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marra,M., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg, K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 807 Std Error: 0.00 Seq primer: -2BM13 rev2 from Amersham High quality sequence stop: 213.
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Vertebrata, Buthería, Rodentía, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            m195510.rl Stratagene mouse kidney (#937315) Mus musculus cDNA clone 519739 5' similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN ;.
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/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 0.00e+00;
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/lab_host="DH10B"
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Best Local Similarity 95.4%;
Matches 308; Conservative
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                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ggcaatccctacatagccaccatttacaaagccgtcggagcctttttgttcggagtctca 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          612 AGGAATAACTACATAGCCACTATTTACAAAGCCATTGGAACCTTTTATTTGGTGCAGCT 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   852 CACTCTTCGTTTTCCATGTACTGCATGCTGTTGTGGCACTTTATCTTCAAGCCAGGATG 911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 259; DB 33; Length 385;
Pred. No. 0.00e+00;
0; Mismatches 60; Indels 1;
                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1810
                                                                                                                                                   MOI:31387
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 375.
Location/Qualifiers
1..385
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Best Local Similarity 84.2%;
Matches 325; Conservative
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Unpublished (1996)
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JOURNAL
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Gaps 13;
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This clone is available royalty-free through LLNL; contact the
IMAGE CONSORTHUM (info@Mage.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 aaccactgagttaaaagggtaactatggtacacacaaaggtgtgccatccaagaaggcata 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 tggggcactgttttggtggaaggcttggagtttttttttaatgagtttagagctattagat 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. [Lases i to 54.2]
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Holtman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Warterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels 13;
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Pred. No. 4.23e-296;
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1314 TCAGCAGCAGAA-GTCTTTAAAGGCTTGTAC-ACCAGG-AAGAAAG-ATGCATCCTC-TT 1260
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122 c
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Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                    house mouse.
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91724432
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BASE COUNT
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JOURNAL
COMMENT
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WashU-Merck EST Project
WashUnderck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 Er from Amersham
High quality sequence stop: 414.
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                                                                                                     Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata; Verebrate; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 54.2)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollann,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkhi,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
AA210789 542 bp mRNA EST 14-FEB-1997
zr90e08.rl Soares NbHTGBC Homo sapiens cDNA clone 682982 5'.
AA210789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by Bento Soares and M. Fatima Bonaldo." /clone="682982"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcatattacatacatgtttatacataagcattacatttttttaataaaatgtatacagg
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 g
                                                                                                                                                                                                                  Wilson, R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.7%;
Best Local Similarity 95.4%;
Matches 308; Conservative
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                                                                                                                                                                                                                                                  Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..542
                                                                                           Homo sapiens
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                                                                            human.
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LOCUS
DEFINITION
ACCESSION
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                                                                                                                                                      AUTHORS
                                                          KEYWORDS
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AA152779 411 bp mRNA EST 11-FEB-1997
AAT78603.11 Stratagene mouse heart (#937316) Mus musculus cDNA clone
603556 5' similar to TR (31161100 G1161100 HYDROGEN
PEROXIDE-INDGCIBLE PROFEIN ;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 ccagccggtgaccatgttcgacaagacgcggctgccgtacgtggccctcgatgtgatttg 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 207.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 123; DB 50; Length 41:
Pred. No. 5.49e-134;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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                                                                                                                                                                                                                                                                            Whitehead Institute/MIT Center for Genome Research; Physically
                           31-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
                                                                                                             STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 119; DB 43; Length 501;
Pred. No. 4.73e-128;
0; Mismatches 26; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/map="188.1 cR from top of Chr5 linkage group"
23..151
                                                                                                                                                                                                                                                                                                                                                                                Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
11-617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rom dbEST (genbank accession R45479)
Location/Qualifiers
                           STS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.025 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(127..151)
. 88 c 117 g
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Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                              Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
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llarity 84.9%;
Conservative
                           501 bp
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Total Vol: 20 ul
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Tris-HCL: 10 mM
                                           human STS WI-15758.
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                                                                                                                                                                                                                                                                                                     Mapped STSs
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MgC12: 1.5 mM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STS size: 129
PCR Profile:
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es 202; Conserv
                                                                                                                                                        collection.
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BASE COUNT
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    13
                                           DEFINITION
ACCESSION
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Matches
                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                          KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHil9W." /clone-"327453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1423 GCCCCACCTGTATACATTTTTATTAAAAAT-GTAATGCTTATGTATAAACATGTATGT 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 aatatgetttetatgaatgatgtttgatttaaatataatacatattaaaatgtatggggg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gococacctgtatacatttttattaaaaaatngtaatgottatgtataaacatgtatgt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, No 63108 Tel: 314 286 1800 Fax: 314 286 1816 Email: estéwatson.wustl.edu Phis clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 981 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 191.
                                                                                                                                                                                                                                                                                                                                                                                                Hiller L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Barsons J., Riffin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The Washu-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                               #1296266
DEMAY-1996 (Rel. 47, Created)
05-MAY-1997 (Rel. 51, Last updated, Version 2)
zc68bll.sl Soares fetal heart NDHH19W Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.7%; Score 120; DB 87; Length 241; Best Local Similarity 99.2%; Pred. No. 1.56e-129; Matches 126; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
complement(<1..>241)
BP; 87 A; 40 C; 36 G; 76 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares fetal heart NbHH19W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
384 aggaatattctgtaatgatgactccat 410
                      449 AGGAGTATTCTGTAATGATGAGTCCAT 475
                                                                                                                             standard; RNA; EST; 241
                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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                                                                                                                                                                                                                                                     327453 37
                                                                                                                        HS368337
                                                                                                                                                 W20368;
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
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(Pharmacia), digested with Not I and cloned into the Not
and Eco RI sites of the modified pT773 vector. Library
constructed and normalized by Bento Soares and M.Patima
1181 CAATCACCAGCCTTGAAAGG-CAGCAGGGTGCCCAGG-TGAAGCTGG-CCTGTTTTCTAA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1037 GAGTCCAGTCAACACATCGCTCCAGTGGTGTTTATAATCAGAAACTCGAGAAAGGCCCAC 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atatatygaaaaagcaatgaggccaaactggagcaatggtcgtaagaagcctggccaatt 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gagtocaactgtgacgtcactccagtggtgtttgtagtcagacactcgagaaaggc-ac 61
                                                     g1862038;

G-MAR-1997 (Rel. 51, Created)

06-MAR-1997 (Rel. 51, Last updated, Version 1)

mx78q01.rl Soares mouse NML Mus musculus cDNA clone 692496 5'

similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contect: Marra W/Wouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108 Tel. 314 286 1800 Fax: 314 286 1810 Email: mousest@vatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:426056 Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            977 ATAAATGGATACGGCAACAAGACCAAATTGCAGTGTGGGGGCGTAAGA-GTCTTGCCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Duboque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 88; DB 91; Length 313;
Pred. No. 6.59e-83;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 A; 58 C; 85 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Scares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project",
                                                                                                                                                                                                                           MM1155742 standard; RNA; EST; 313
AA237956;
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Best Local Similarity 66.5%;
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished.
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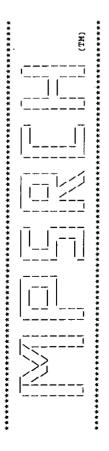
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double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatina
                                                                                                                                                                                                                                                                                                                                                                              AA237956 313 bp mRNA EST 03-MAR-1997 mx78g01.rl Soares mouse NML Mus musculus cDNA clone 692496 5' similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Leh., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
182 agaattttccgggttggaaggccaactggccttcttggatttcccct-caatcccttggc 240
                                                 858 AAGAGTGGCCTGAATAGAAGGACAACCTGCCTTCCTTAACTCTTTCTGCATTCCCTCGAC 799
                                                                                                         241 ataaggagttetteatattggeattaatggagttggattttgaacagteteggttataga 300
                                                                                                                                         Gaps
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Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
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Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 313;
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0; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/lab_host="DH10B"
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Best Local Similarity 66.5%;
Matches 208; Conservative
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C
                                                                                                                                                                                                                   301 gatgccagaaatg 313
                                                                                                                                                                                                                                                                       738 CATCCAAGAAGIG 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
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Search completed: Thu Nov 6 10:41:38 1997 Job time: 577 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith Waterman algorithm MPsrch_pp Run on:

Tue Nov 4 10:18:50 1997; MasPar time 7.05 Seconds 495.371 Million cell updates/sec Fabular output not generated.

>US-08-842-827-2 (1-284) from US08842827.pep 2125 Description: Perfect Score:

1 MFDKTRLPYVALDVLCVLLA.......HTTLHETPTTGNHYPSNHQP 284 Sequence:

PAM 150 Scoring table:

101610 seqs, 12294212 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-geneseq28 Database:

liparil 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part16 17:part16 17:part17 18:part18 19:part18 20:part21 21:part19 20:part21

Variance 149.470; scale 0.225 Mean 33.575; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

80	۱ ـ	0	0	0	0	0	0	0	_	-	_	-	_	ᅼ	ᅼ	=	=	=	-	-
	e-0	07e+00	07e+00	07e+0(07e+00	07e+00	07e+00	07e+00	61e+0	59e+0;	59e+0	21e+0	21e+0	21e+0	21e+0	55e+0	55e+0	55e+0	55e+0	55e+01
Pred.	9.69e-01	6.07	6.07	6.07	6.07	6.07	6.07	6.07	1.61	2.59	2.59	2.21	2.21	2.21	2.21	3.55	3,55	3.55	3.55	3.55
Description	Prod. cDNA insert of	Heart calcium/calmodu	Cyclic-GMP stimulated	Prod. of cDNA insert	Hippocampus calcium/c	Cyclic-GMP stimulated	Rabbit skeletal calci	Rabbit seletal muscle	Rat dorsal root gangl	H. pylori cell envelo	H. pylori cell envelo	Sequence of human alp	Pea proton transport	Alpha subunit of inte	Alpha 6A integrin sub	Alternatively spliced	Product of alternativ	Protocadherin clone 4	Human protocadherin-4	Alpha 6B integrin sub
QI	R28412	W11257	R69733	R28413	W11256	R69732	R73055	P95645	W04217	W20522	W20587	R52832	R53463	R55272	R28821	R87153	R58912	R87147	R58907	R28822
8	ស	20	13	'n	20	13	13	Н	18	77	21	10	10	10	'n	11	11	17	11	J.
Length DB	634	564	564	564	634	634	1873	1873	397	186	254	466	. 563	1073	1073	836	836	904	904	1091
% Query Match	5.3	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.3	4.3	4.3
Score	.113	102	102	102	102	102	102	102	96	66	66	94	94	94	94	91	91	91	91	91
Result No.	н	61	m	7	'n	Q	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20

3.03e+01 3.55e+01 4.15e+01 4.15e+01			4.85e+01 4.85e+01 4.15e+01	144.6		5.67e+01 5.67e+01 5.67e+01 5.67e+01
Human SMCY protein. Encoded by full-lengt H. pylori transporter H. pylori transporter	drener drener drener	alpha-1C alpha-1C alpha-1C	Human alpha ic adrene Human alpha ic adrene Encoded by Hepatitis		H. pylori transmembra G-protein coupled cow G-protein coupled cow	ABF-A from A. niger. Vitamin K dependent c Rubella virus strain Murine adenylate cycl
W13905 R34468 W20268 W20935	M03/14 R53073 R85944 R58680	R90037 R58679 R90038	R73604 R73603 R34467	R34478 W20801 W03713	0000	R27575 R28954 R73916 R99251
21 21 21 21 21 21 21 21 21 21 21 21 21 2	9 4 1	118			21 16 19	13 13
1539 3011 205 270	4 4 4 4 6 6 6 6 6 7 9 9 9	4 4 4 6 6 6 6 6 6 6	4 4 4 7 4 4 6 7 0 7 0	4 4 4 4 4 4 4 4 4 4 9 9 9 9 9 9 9 9 9 9	375 375	758 1063 1353
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22 22 24 24	27 27 28 24	30 30 30 30 30 30 30 30 30 30 30 30 30 3	3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	3336	6 4 4 9 6 0 1 0	4 4 4 4 2 6 4 6

ALIGNMENTS

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A copy cione from the hippocompus cona library that had been a contains a 2.7 kb insert. The contains a 2.7 kb insert was excised from the lambda clone to yield two relevant fragments. These two fragments of the asbacione was designated pocamH3EF. Although this contains, hybridises to the bowine cam PDE 61 kD cDNA, sequence analysis revealed that it appears to be a prod. of a different Cam PDE gene. Plasmid pocamH3EF contains what may be the entire ORF and would encode a protein approx. 75 percent homologous with the protein encoded by contain sergion between nucleotide 80-100 of pocamH3EF is uncertain. This area is 5, to the initiator methionine codon and thus does not effect the ORF.
                                                                                                                                                                                                                                                                                                                                                                New DNA encoding mammalian cyclic nucleotide phospho-di:esterase - and desived vectors and host cells, useful for screening cpds. for inhibitory or activating activity example 7; Page 109; 133pp; English.
                                                                 19-WAR-1993 (first entry)
Prod. cDNA insert of pcanH3EF, homologous to CaM PDE.
Calcim/ calmodulin; stimulated; cyclic; nucleotide; bovine;
                                                                                                                                                                                                                                                                                       Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK; WPI; 92-382051/46.
  T 1
R28412 standard; Protein; 634 AA.
                                                                                                                                                                                                    29-OCT-1992,
20-APR-1992; U03222,
19-APR-1991; US-688356,
(UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 AA;
                                                                                                                                     phosphodiesterase
                                                                                                                                                                                                                                                                                                                                          N-PDSB; 030187
                                                                                                                                                           Homo sapiens.
WO9218541-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
RESULT
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Score 113; DB 5; Length 634; Pred. No. 9.69e-01; 27; Mismatches 31; Indels 4; Gaps Query Match 5.3%; Best Local Similarity 25.3%; Matches 21; Conservative

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182 ddalkfifyelltrydlisrikipisalvsfv-ealevgysk--hknpyhnlmhaadvtg 238 | :::|::| | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :

US-08-842-827-2.rag

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alter the carboxy terminus of the protein encoded by the ORF.

pcamH3EF cDNA can encode a protein of 634 residues, and assuming
the 5' end of pcamHella cDNA 1s the same as that of the 5' end of
pcam3HEF (5' to nucleotide 610), pcamHella can encode a 709 residue
protein. These divergent 3' ends may be the consequence of alternative
splicing, lack of splicing, or unrelated DNA sequences being juxtaposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding mammalian cyclic nucleotide phospho-disesterase and derived vectors and host cells, useful for screening cpds.

Fand derived vectors and host cells, useful for screening cpds.

Fan approx. 2.4 kb fragment of pcamHist was used to screen an upprox. 2.4 kb fragment of pcamHist was used to screen a human heart cDNA library to yield two plaques which hybridised to the pcamHist probe. The Blueskript SF plasmid pcamHella was excised in vivo from one of these clones. Sequence analysis of pcamHella showed that the insert began at nucleotide 610 of pcamHist and was nearly identical to nucleotide 2066, at which point the DNA sequence diverged from that of pcamHist. The cDNA insert of pcamHella continued for ca. 0.6 kb. The consequence of this divergence is to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 DESIKYPYKEDTIPYALLGGIIIPPSIIVIILGETLSV-YCNLLHSNSFIRNNYIATIYK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 dhalkfifyelltrydlisrfkipisalvsfv-ealevgysk--hknpyhnlmhaadvtq 93
                                                                                                                                                                                                                                                                  Example 7: Columns 117-122; 69pp; English.

083902 encodes R69733 the human cyclic-GMP stimulated nucleotide phospho-diesterase (CaM PDE) clone pecan-Hella. Eukaryotic cells that express Cam PDE clone becan-Hella. Eukaryotic cells modulate CaM PDE activity. CaM PDEs are involved in regulating the transmission of information from hormones, neurotransmitters or other systems that use cyclic nucleotides as messengers.

Antibodies raised against CaM PDE can be used for enzyme purifon, or determination.
                                                                                                                                                               New nucleic acid encoding cyclic-GMP stimulated nucleotide phospho-di-esterase - and related vectors and transformed celuseful for screening cpds. for phospho-di-esterase modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 102; DB 13; Length 564;
Pred. No. 6.07e+00;
27; Mismatches 32; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of cDNA insert of pcamHella. m/ calmodulin; stimulated; cyclic; nucleotide; bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 102; DB 5; Length 564; Pred. No. 6.07e+00;
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                                                                                           Sonnenburg WK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T
R28413 standard; Protein; 564 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 tvhyllyktgvanwlteleifai 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AIGTFLFGAAASOSLTDIAKYSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.1%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.8%;
Best Local Similarity 24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   during the cloning process
Sequence 564 AA;
                                                                                        Charbonneau H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1992.
20-APR-1992; U03222.
19-APR-1991; US-688356.
(UNIW ) UNIV WASHINGTON.
                                                           (UNIW ) UNIV WASHINGTON
                                    20-APR-1992; US-872644
                                                                                     Beavo JA, Charbonr
WPI; 95-090205/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 92-382051/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphodiesterase
                                                                                                                                           N-PSDB; 083982
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WO9218541-A.
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                                                                                                                                                                                                                                                    activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7: Column 117-12; 68pp; English.

This sequence represents the calcium/calmodulin dependent
This sequence represents the calcium/calmodulin dependent
This sequence represents the calcium/calmodulin dependent
This cDNA insert was isolated from human heart mRNA. The cyclic
This cDNA insert was isolated from human heart mRNA. The cyclic
This cDNA insert was isolated from human heart mRNA. The cyclic
This cDNA insert was isolated from human heart mRNA. The cyclic
This cDNA insert was isolated from human heart mRNA. The cyclic
This cDNA insert was isolated from human heart mRNA. The cyclic
This cDNA insert was cappared from the cyclic micleotides.

The control of the cellular concentration of cyclic nucleotides. The PDEs are, in turn, regulated by transmembrane signals or second messenger.

Tole in regulating the flow of information from extracellular hormones, neurotransmitters, or other signals that use the cyclic nucleotides as messengers. PDEs are present in most of the cells and tissues of curvatual contentration of CAMP, and/or cGMP. The cDNA encoding this sequence can therapeutic and diagnostic uses. This protein may also be useful for clanary and the antibody production.

This combinant can be useful for antibody production.

This combinant can be useful for antibody production.
                                                                                                                                                                                                                                      Heart calcium/calmodulin dependent phosphodiesterase.
Cyclic GWP stimulated phosphodiesterase; cGs-pB; bovine; brain; cAMP;
adrenal gland; transmembrane signal; extracellular hormone; antibody;
neurotransmitter; cGMP; calcium/calmodulin dependent phosphotriesterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 dhalkfifyelltrydlisrfkipisalvsfv-ealevgysk--hknpyhnlmhaadvtg 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 102; DB 20; Length 564;
Pred. No. 6.07e+00;
27; Mismatches 32; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclic-GMP stimulated nucleotide PDE clone pcam-Hella. Cyclic-GMP stimulated nucleotide phospho-diesterase; antibodies; human; hormones; neurotransmitters; transmission regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding cGMP-stimulated phospho:di:esterase - for prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sonnenburg WK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme purification; clone pcam-Hella.
                                                                                                                                  T 2
W11257 standard; Protein; 564 AA.
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239 tvhyllyktgvanwlteleifai 261
                                    101 AIGTFLFGAAASQSLTDIAKYSI 123
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R69733 standard; Protein; 564
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Sest Local Similarity 24.1%;
Atches 20; Conservative
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charbonneau H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-1991; US-688356.
20-APR-1992; US-872644.
29-AUG-1994; US-297494.
(UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                         688356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beavo JA, Charbonn
WPI, 97-033573/03.
                                                                                                                                                                                                                                                                                                                                            CaM-PDE; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T51117
                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-1991;
19-APR-1991;
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US5389527-A.
                                                                                                                                                                                                               17-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R69733;
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Matches

a à a à RESULT
ID R6
DT 110
DE CY
KW CY
KW PI
KW PU
PD U
PD U
PD I
PD I

'n

4; Gaps

transmission regulation;

Matches

g ö 셤 ö

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182 dhalkfifyelltrydlisrfkipisalvsfv-ealevgysk--hknpyhnlmhaadvtq 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         083981 encodes 869732 the human cyclic-GMP stimulated nucleotide phospho-diesterase (CaM PDE) clone poamH3BF. Eukaryotic cells that express CaM PDE and used to screen cpds. for the ability to modulate CaM PDE activity. CaM PDEs are involved in regulating the transmission of information from hormones, neurotransmitters or other systems that use cyclic nucleotides as messengers. Antibodies raised against CaM PDE can be used for enzyme purifor, or determination.
                                                                                                                                                                                                                                                                   related vectors and transformed cells, for phospho-di-esterase modulating
                                                                                                                                                                                                                                             New nucleic acid encoding cyclic-GMP stimulated nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102; DB 13; L. Pred. No. 6.07e+00; 27; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-NOV-1995 (first entry)
Rabbit skeletal calcium channel (alpha)1-subunit.
Calcium channel; (alpha)1 subunit.
oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label potential cAMP-dependent phosporylation odified_site 1502
                                                                                                                                                                                                                                                                                                                       Example 7; Columns 109-114; 69pp; English.
                                                                                                                                                                                     Sonnenburg WK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label - IIF7 monoclonal antibody epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Fotential N-glycosylation site
fodified_site 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                         enzyme purification; clone pcamH3EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R73055 standard; Protein; 1873 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 AIGTFLFGAAASQSLTDIAKYSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 4.8%;
Local Similarity 24.1%;
les 20; Conservative
                                                                                                                                                                                                                                                                 phospho-di:esterase - and useful for screening cpds.
                                                                                                                                                                                 Beavo JA, Charbonneau H, WPI; 95-090205/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Ala
/note= "In Tanabe et al"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "In Tanabe et al"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "In Tanabe et al"
                                                                                                                      19-APR-1991; US-688356.
20-APR-1992; US-872644.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc_difference 1808
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/label= secabove
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Modified_site 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            = see above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     see above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified_site 1:
/label= see above
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                                                                                                                                                                                                                          N-PSDB; 083981
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                                             Homo sapiens.
US5389527-A.
                                                                                                       19-APR-1991;
                                                                                  14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- Thr
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                                                                                                                                                                                                                                                                                                          activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcontinent entryine.

Transport of the sequence represents the calcium/calmodulin dependent

This cDNA insert was isolated from human hippocampus mRNA. The cyclic

This cDNA insert was isolated from human hippocampus mRNA. The cyclic

This cDNA insert was isolated from human hippocampus mRNA. The cyclic

C cyclic nucleotide phosphodiesterases (PDES) catalyse the hydrolysis of 3', 5'

C cyclic nucleotide monophosphates. The PDES are therefore important in the

CC cyclic nucleotides. The PDES are therefore important in the

CC control of the cellular concentration of cyclic nucleotides. The PDES

This in turn, regulating the flow of information from extracellular hormones,

CC in regulating the flow of information from extracellular hormones,

CC intracellular calcium, which leads to a decreased intracellular

CC concentration of CAMP, and/or cAMP. The CDNA encoding this sequence can

CC therepotutic and diagnostic uses. This protein may also be useful for
                                                                                                                                                                                                                                                                         17-180. (first entry)
17-180. (first entry)
Hippocampus calcium/calmodulin dependent phosphodiesterase #2.
Gyolic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; cAMP; adrenal gland; transmembrane signal; extracellular hormone; antibody; neurotransmitter; cGMP; calcium/calmodulin dependent phosphotriesterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
    ε,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R69732;
11-OCT-1995 (first entry)
Cyclic-GMP stimulated nucleotide PDE clone pcamH3EF.
Cyclic-GMP stimulated nucleotide phospho-diesterase; antibodies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cGMP-stimulated phospho:di:esterase - for prodn. recombinant enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 102; DB 20; Length 634
Pred. No. 6.07e+00;
27; Mismatches 32; Indels
  27; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sonnenburg WK;
                                                                                                                                                                                                                   J. 5
W11256 standard, Protein, 634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R69732 standard; Protein; 634 AA
                                                                                                                  94 tvhyllyktgvanwlteleifai 116
                                                                                                                                                           101 AIGTFLFGAAASQSLTDIAKYSI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 tvhyllyktgvanwlteleifai 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic antibody production
Sequence 634 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 24.1%;
Matches 20; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beavo JA, Charbonneau H, WPI; 97-033573/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-1991, 688356.
19-APR-1991; US-688356.
20-APR-1992; US-872644.
29-AUG-1994; US-297494.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                 CaM-PDE; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T51116
20;
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RESULT

셤 ö 셤

Gaps

Indels

Length 634;

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New DNA encoding alpha-2 subunit of animal calcium channel - also new protein product and eukaryotic cells for testing cpds. for calcium agonist or antagonist activity
Disclosure; page 16-1 to 18-3; 68pp; English.
Also used to diagnose Lambert-Eaton syndrome by reacting test serum with alpha-1 and alpha-2 subunits. Labelled fragments can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 PYKEDTIPYALLGGIIPF-SIIVIILGETLSVYCNLLHSNSFIRNNYIATIYKAIGTFL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        821 piraesvrngilgyfdiaftsvftveivlkmttygaflhkgsfcrnyfnildllvvavsl 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  821 piraesvrngilgyfdiaftsvftveivlkmttygaflhkgsfcrnyfnildllvvavsl 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 PYKEDTIPYALLGGIIIPF-SIIVIILGETLSVYCNLLHSNSFIRNNYIATIYKAIGTFL 106
three (see FT) also result in AA changes (see R73055 FT). The deduced As sequence yields a calculated Mr of 212,143,in contrast to the observed Mr 155K-176K, previously reported by others using SDS polyacrylamide gel electrophoresis. The AA sequence is 99.8% internal repeated sequence regions. The AA sequence is 99.8% internal repeated sequence regions. It has been proposed that the segments of the four internally repeated regions represent 24 transmembrane segments. A eukaryotic cell expressing a chimaeric consisting of chok in which the first CDNA is selected from the gp. consisting of condoss a protein that has the AA sequence in R73055 but with the Tanabe et al substitutions indicated in FT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W04217;
32.NOV-1996 (first entry)
Rat dorsal root ganglion Pax receptor.
ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist;
ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist;
paragonist; pelipersy; cognition; emesis; pain; asthma;
peripheral vascular disease; hypertension; irritable bowel syndrome;
premature ejaculation; cystitis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Score 102; DB 13; Length 1873;
Pred. No. 6.07e+00;
22; Mismatches 39; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-1989:
04-APR-1988: 001408.
(SALK) Salk Inst for Blol Stud.
Ellis SB, Williams ME, Harpold MM, Schwartz A, Sartor J;
WPI: 89-32426/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabbit seletal muscle alpha-1 sub-unit gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 8
P95645 standard; protein; 1873 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 FGAAASQSLTDIAKY-SIGR-LRP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               881 ismglesstisvvkilrvlrp 904
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W04217 standard; Protein; 397 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   4.8%;
Local Similarity 23.8%;
nes 20; Conservative
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WO8909834-A.
                                                                                                                                                                                                                                                                                                                                             1873 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1873 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeletal muscle
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                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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            8888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1: 32pp; English.
The cDNA sequence Q87978 is consistent with an approx 6,500 nt DHP receptor (alpha)1 mRNA. It is 948 identical to the cDNA sequence encoding the DHP receptor reported by Tanabe et al., Nature, 328:313-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding alpha-1 and alpha-2 calcium channel sub-unit(s) for detecting calcium channel agonists/antagonists or Lambert-Eaton syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams ME;
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Brenner R, Ellis SB, Harpold MM, Schwartz A,
                                                                                                                                                                                                                                                                                                            /label transmembrane region
Protein 89..108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1041..1065
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                                                                                                                                                                                                                                                                                                                              Protein ...../label see above 121..139
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835.854
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/label- see above
893.912
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/label- see above
931..950
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/label- see above
524..542
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/label= see above
562..581
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/label= see above
52..70
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04-APR-1989; US-603751.
13-JUL-1992; US-914231.
                                                                                                               1772
                                                                                                                                          /label= see above
Modified_site 1854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region 16
/label- see above
   Modified_site 15
/label= see above
                                                                                    'label- see above
                                                                                                                                                                                                /label- see above
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/label- see above
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/label- see above
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/label= see above
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                                                      Modified_site
                                                                                                                  Modified site
                                                                                                                                                                                                                        Modified_site
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                                                                                                                                                                                                                                                                                       Region
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protein.
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                                                                                                                                                                       W20587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Particolater pylori nucleic acid sequences and related polypeptide(8) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter and to detect Helicobacter claim 56; Page 682; 1481pp; English.

This sequence is a H. pylori cell envelope protein.

This sequence is a H. pylori cell envelope protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide blinding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori life cycle activators of interest in the predicted coding regions fefined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by POR amplification for recombinant polypeptide Squence 186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori cell envelope protein 4826401 aa. Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                              Screening cods. useful in treating epilepsy, cognition, emesis, pain, asthma, peripheral vascular disease, hypertension, etc.

Claim 1; Fig 3; S2pp; English.

The amino acid sequence (M44217) of rat dorsal root ganglion P2x receptor was deduced from a cDNA clone (T33854) isolated from a cDNA ibrary. P2x receptors (see also W04215-16 and W04218) are ligand-gated ion channels that open upon binding of extracellular ATP. Recombinant P2x receptors can be produced in prokaryotic or eukaryotic, pref. mammalian, host cells. Their widespread distr.
                                                                                                                                                                                                                                                                                                                                                   P2x receptors useful for the screening of new cpds. (agonists or antagonists) for the treatment of a number of pathological states.
                                                                                                                                                                   DNA encoding ATP P2x receptors of the purinoceptor family - for
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96; DB 18; Length 397;
Pred. No. 1.61e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 tvlcdiillnflkgadhykarkfeevtettlkgtastnpvfasdg 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 AILVAVYVSDFFKERTSFKERK-EEDSHTTLHETPTTGNHYPSNH 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASTR ) ASTRA AB.
Berglindh OT, Smith D, Wellgaerd BL;
WPI; 97-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W20522 standard; Protein; 186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUL-1997 (first entry)
                              07.DEC-1995.
24.AAX-1995; E01968.
27.WAX-1994; GB-010664.
09-FEB-1995; GB-002480.
(GLAX ) GLAXO GROUP LTD.
BUELL GN. VALETE S;
WPI; 96-030561/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-1996, 009122.
06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori. WO9640893-A1.
                                                                                                                                                                                                                                                                                                                                                                                      397 AA;
                                                                                                                                                   N-PSDB: T33854
Rattus sp.
WO9533048-A2.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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DB 21; Length 186;

4.4%; Score 93;

Query Match

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H. pylori infection or to identify H. pylori polypeptide binding
compounds, useful as potential H. pylori life cycle activators or
cinhibitors. The genomic sequence of H. pylori (Arcc 55679) was
determined from overlapping contigs generated by mechanically
shearing the bacterial DNA. The sequences were analysed for ORF of
at least 180 nucleotides, and the predicted coding regions defined
by computer evaluation. To identify likely H. pylori antigens for
vaccine development, the amino acid sequences predicted from
various ORF were analysed for significant homology to other known
c or exported membrane proteins. Having identified and determined
the sequences of interest, particular regions can be isolated from
H. pylori by PCR amplification for recombinant polypeptide
Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacterial Claim 56; Pages 1018-1019; 1481pp; English.
The present sequence is a Helicobacter pylori cell envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 qsivyallgtlvlsitiipvv-s-sl-vlkatphsetfl-trflnriyaplleff 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 DIPPALLGGIIIPFSIIVILIGETLSVYCNLLHSNSFIRNNYIATIYKAIGFFL 106
                                                                                                               52 DIIPPALLGGIIIPFSIIVIILGETLSVYCNLLHSNSFIRNNIATIYKAIGTEL 106
                                                                                                                                                                                                                                                                                             14-Jul-1997 (first entry)
H. pylori cell envelope protein, Olae2200lorf2.
Vaccine; prevention; treatment; infection; identification; banding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;
                                                                                  31 qsivyallgtlvlsitiipvv-s-sl-vlkatphsetfl-trflnriyaplleff 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hartig PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%; Score 93; DB 21; Length 254; 9.1%; Pred. No. 2.59e+01; tive 20; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha 1C; adrenergic receptor; antagonist; neuroreceptor.
Homo sapiens.
                             Indels
  Pred. No. 2.59e+01;
20; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gluchowski C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-1994 (first entry)
Sequence of human alpha 1 C adrenergic receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Branchek TA, Chiu G, Forray CC,
                                                                                                                                                                                                                   T 11
W20587 standard; protein; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R52832 standard; Protein; 466 AA.
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Best Local Similarity 29.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996.
06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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13-NOV-1992; US-975867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASTR ) ASTRA AB.
Berglindh OT, Smi
WPI; 97-052306/05.
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                                                                                                                                                                                                                                                                                                                                                                                                            inhibiťor; àuo
cell envelope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9640893-A1.
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Alpha subunit of integrin cell surface receptor. Integrin; alpha; beta; subunit; glycoprotein; heterodimer; transmembrane; extracellular matrix; cell signalling; cytoskeleton; behaviour; signal transduction; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing presence of abnormal epithelial tissue in vitro -
utilises monoclonal antibodies to alpha6 beta4 cell surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note "This sequence is conserved in all but the
                                                                                                                                                                                                                             misc_binding 230..238
/note= "Sequence weakly homologous with cation binding site of other integrin alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "This sequence closely resembles the cleavage site of other integrin O chains." misc_feature 1040..1044
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Putative cation binding site." misc_feature 899..903
                                                                                                                                                                                                                                                                                                                                   /note- "Putative cation binding site." misc_binding 386.394
                                                                                                                                                                                                                                                                                                                                                                                /note- "Putative cation binding site." nisc_binding 441...449
                                                                                                                                                                                                          Location/Qualifiers
       7T 14
R55272 standard; Protein; 1073 AA.
R55272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1054 yhkaeihaqpsdkerltsd 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 SHTT-LHEIPITGNHYPSN 281
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Best Local Similarity 25.3%;
Matches 20; Conservative
                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                  324..332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-1987; 016552.
19-FEB-1987; US-016552.
04-JAN-1989; US-293384.
01-OCT-1990; US-591105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quaranta V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (QUAR/) QUARANTA V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1073 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94-191533/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KAJI/) KAJIJI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q65673
                                                                                                                                                                                                                                                                                                                                                                                                      misc_binding
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                  misc_binding
                                                                                                                                                                                                                                                                                                                                                           misc_binding
                                                                    27-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5320942-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kajiji S,
                                                                                                                                                                                                                                                                                               subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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       RESULT
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                            셤
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                            Selectively to alphalic adrenergic receptor to inhibit contraction of prostatic tissue

Example; Page 53-55; 69pp; English.

The liventors claim a method of treating benign prostatic
The liventors claim a method of treating benign prostatic
The liventors claim a method of treating the prostatic
The properplasia which comprises administering a therapeutically
effective amount of a compound which binds to a human alpha-1c
adrenergic receptor with a binding affinity greater than ten-fold
higher than the binding affinity with which the compound binds to a
creceptor. The example concerns a protocol for the determination of
the potency of alpha-1 antagonists. Cell lines were prepd, by
transfecting the cloned cDNA or cloned genomic DNA or constructs
conty both genomic DNA and cDNA encoding human alpha-adrenergic
conty both genomic DNA and cDNA encoding region and 5' and 3'
UTRS were cloned into the BamHI and Clai sites of the
ENJ:IR. For alpha-1B, the entire coding region and 5' and 3'
UTRS were cloned into the ECORI site of ECEXY-3 eukaryotic expression
vector. For alpha-1C, the entire coding region and 5' and 3'
UTRS were cloned into the KpnI site of the polylinker-modified
DUTRS were cloned into the Romi site of the polylinker-modified
CUTRS were cloned into the Romi site of the polylinker-modified
DUTRS were cloned into the Romi site of the polylinker-modified
CUTRS were cloned into the Romi site of the polylinker-modified
DUTRS were cloned into the Romi site of the polylinker-modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 YCMLFVALYLQARMKGDWARLERPT-LQFGLVAVS-IYVGLSRVSDYKHHWSDVL-TGLI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 llgvilgglilfgvlgnilvilsvachrhlhsvthyyivnlavadllltstvlpfsaife 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94; DB 10; Length 563;
Pred. No. 2.21e+01;
20; Mismatches 31; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
Treating benign prostatic hyperplasia - with cpds. which bind selectively to alphalC adrenergic receptor to inhibit contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proton transport adenosine tri:phosphatase protein and its coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tri:phosphatase
Claim 2; Page 6-7; 8pp; Japanese.
This sequence is a proton transport adenosine triphosphatase
protein from the plasma membrane of Pisum sativum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.21e+01;
23; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pea proton transport adenosine triphosphatase.
Proton transport adenosine triphosphatase; H+ATPase; pea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene - for preparation of pure proton transport adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.4%; Score 94; DB 10; Best Local Similarity 27.0%; Pred. No. 2.21e+01 Matches 20; Conservative 23; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 563 AA.
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29-SEP-1992; JP-260333.
(YAWA ) NIPPON STEEL CHEM CO.
(XAWA ) NIPPON STEEL CORP.
WPI: 94-172755/21.
N-PSDB; Q63601.
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Best Local Similarity 27.0%;
Matches 20; Conservative
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R53463 standard; Protein; 9
R53463;
18-JAN-1995 (first entry)
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234 QGALVAILVAVYVS 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 AA;
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Example 5; Figure 6: 34pp; English.

Integrins are heterodimers commissed of alpha and beta subunits, that are non-covalently associated transmembrane glycoproteins. Il alpha chains and 6 beta chains have been recognised in man. Each alpha subunit tends to associate with only one type of beta subunit but there are several exceptions. Integrins mediate (in part) the interaction of cells with the extracellular matrix, forming a link between the extracellular matrix and the cytoskeleton. They may environment, affecting cell behaviour. This sequence is the alpha6 subunit of an alpha6 beta4 integrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha 6A integrin subunit.
Human; alpha 6A; alpha 6B; integrin; cell surface receptor; adhesion;
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Pred. No. 2.21e+01;
23; Mismatches 29; Indels 7;
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7;

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Disclosure; Page 69-73; 115pp; English.

The sequences given in R28821-22 are the human alpha 6A and 6B integrin subunits. Integrins are a family of cell surface receptors integrin subunits. Integrins and a family of cell surface receptors which serve cellular adhesion functions. These receptors form a link between the extracellular components. Each integrin receptor is a heterodimer comprised of an alpha and a beta subunit. Each alpha subunit tends to associate with only one type of beta subunit but there are several exceptions to this rule. These integrins correspond to the laminin receptor. The cytoplasmic domain of the 6A and 6B integrins differs from previously isolated alpha 6 integrins. The buman alpha 6B was isolated from human choriocarcinoma cell line JAR squence 1073 AA;
extracellular matrix; cytoskeleton; heterodimer; laminin receptor; immunoprecipitation; JAR; choriocarcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integrin alpha sub-unit cytoplasmic domain polypeptide(s) - used for prodn. of antibodies and in detection of integrin sub-units in body samples
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Binding_site 441.449
/note= "Putative cation binding domain"
Binding_site 441.449
/note= "Putative cation binding domain"
Binding_site 1040...044
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/note= "Conservered in virtually all integrins"
W0921964-7-A.
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/label 61ycosylation_site
Binding_site 230..238
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                                                  Location/Qualifiers
                                                                 Domain 1012..1037
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27-APR-1992; U03527.
23-MAY-1991; US-695564.
(SCRI ) SCRIPPS RES INST.
Quaranta V, Tamura RN;
WPI: 92-396799/48.
N-PSDB: Q31188.
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                                 Homo sapiens.
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Search completed: Tue Nov 4 10:20:24 1997 Job time: 94 secs. 1054 yhkaeihaqpsdkerltsd 1072 264 SHTT-LHETPTTGNHYPSN 281

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Nov 4 10:17:27 1997; MasPar time 10.95 Seconds 749.603 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score: Title:

>US-08-842-827-2 (1-284) from US08842827.pep 2125 1 MFDKTRLPYVALDVLCVLLA......HTTLHETPTTGNHYPSNHQP 284 Sednence:

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir51 Database:

1:anol 2:anol 3:anol 3:anol 4:anol 5:unanol 6:unanol 7:unanol 8:unanol 9:unanol 10:unanol 11:unanol 12:unanol 14:unanol 15:unanol 16:unanol 16:una

Mean 45.994; Variance 109.223; scale 0.421 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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S70114 *type complete
hypothetical protein YDR284c - yeast (Saccharomyces
cerevisiae)
#formal_name Saccharomyces cerevisiae
24-404-1996 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996

ORGANISM DATE

RESULT ENTRY TITLE

MDM1 protein - yeast 6.09e+00 genome polyprotein - 4.79e+00 polyprotein - 4.79e+00 polyprotein - 4.79e+00 polyprotein - dongue 6.09e+00 hypothetical protein 7.73e+00 phenylalaninetRNA 9.79e+00 NADH dehydrogenase (7.73e+00 NADH dehydrogenase (7.73e+00 purinoceptor P2X - r 73e+00 gene P2X3 protein - 7.73e+00 probable cadmium-tra 9.79e+00 probable cadmium-tra 9.79e+00 probable olfactory r 1.24e+01 trypsin (EC 3.4.21.4 1.24e+01 probable membrane pr 1.24e+01 probable membrane pr 1.24e+01 probable membrane pr 1.56e+01 cell fusion protein 1.24e+01 probable membrane pr 1.56e+01 probable membrane pr 1.56e+01 probable membrane pr 1.56e+01 probable membrane pr 1.56e+01 h+-transporting ATPa 1.24e+01 h+-transporting ATPa 1.24e+01 virA protein - Agrob 1.97e+01	ENTS Tokasa (Saccharomyces Tokasa - yeast (Saccharomyces Myces cerevisiae Lrevision 06-Sep-1996 #text_change Tokas Library, August 1995 Trevisiae cosmids 8166, 9787, 9717, and E E Tokasa - Weight 31586 #checksum 1196	8; DB 11; Length 274; 1.94e-11; matches 57; Indels 9; liighlrpdfvdrcipdlqkmsdsds
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ACCESSIONS

GENETICS

SUMMARY

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#authors Kessler, A.C.; Haase, A.; Reeves, P.R.
#Journal J. Bacteriol. (1993) 175:1412-1422
#title Molecular analysis of the 3,6-dideoxyhexose pathway genes of Yersinia pseudotuberculosis serogroup IIA.
                                                                                                                                                                                                                                                                                 Rauschenbach, R.; Isernhagen, M.; Noeske-Jungblut, C.;
Boidol, W.; Siewert, G.
Submitted to the EMBL Data Library, March 1993
Cloning, sequencing and expression of the gene for cytoch
P450meg, the steroid 15beta-monocxygenase from Bacillus
megaterium ATCC 13368.
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                                                                                                                                                       hypothetical protein 2 - Bacilius megaterium #formal name Bacilius megaterium 06-Reb-1995 #text_change 06-Reb-1995 #text_change 06-Reb-1995
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#formal_name Yersinia pseudotuberculosis
21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
23-Mar-1995
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# #length 216 #molecular-weight 24946 #checksum 8213
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Pred. No. 2.37e-01;
16; Mismatches 16; Indels
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NADH-ubiquinone oxidoreductase chain 2
#formal_name mitochondrion Xenopus laevis #common_name African clawed frog
28-Reb-1996 #sequence_revision 28-Feb-1986 #text_change 09-Sep-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *authors Roe, B.A.; Ma, D.P.; Wilson, R.K.; Wong, J.F.H.
#journal J. Biol. Chem. (1985) 260:9759-9774
#title The complete nucleotide sequence of the Xenopus laevis #cross-references MUID:85261388
                                                                                                                                                                                                                                           *length 289 #molecular-weight 33514 #checksum 4703
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                                                                                                                                                                                                                                                                                     Score 181; DB 11; Length 289;
Pred. No. 1.86e-10;
65; Mismatches 98; Indels 18;
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                                     Fulton, L. submitted to the EMBL Data Library, May 1996 The sequence of S. cerevisiae cosmid 9819.
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                                                                                                                                                                             ##cross-references EMBL:U51031
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Best Local Similarity 27.0%;
Matches 67; Conservative
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SGC1
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##molecule_type_DNA
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ACCESSIONS REFERENCE

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This sequence was derived from multiple, partial, alternatively
spliced mRNAs. The sequence shown is a composite representing the
longest possible splice form. Two splice forms lead to premature
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                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4628-4632
Molecular diversity of L-type Ca2+ channel transcripts in
human fibroblasts.
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31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                  #formal_name Homo sapiens #common_name man
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
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#region alternatively spliced segment 2\
#region alternatively spliced segment 3\
#region alternatively spliced segment 4\
#region alternatively spliced segment 5
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#length 370 #molecular-weight 35778 #checksum 3813
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Pred. No. 1.41e+00;
18; Mismatches 31; Indels
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34; Mismatches 56; Indels
calcium channel protein type L - human
                                                                                                                                                                                                    #accession A45290
##molecule_type mRNA
##residues 1-220 ##label SOL
##cross-references NCBIN:105570; NCBIP:105571
##experimental_source fibroblast
##note this sequence is inconsistent
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##molecule_type protein
##residues 1-370 ##label VEL
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Best Local Similarity 31.3%;
Matches 25; Conservative
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Best Local Similarity 23.2%;
Matches 29; Conservative
                                                                                                            Soldatov, N.M.
                                                      28-Apr-1995
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Danabe, T.; Takeshima, H.; Mikami, A.; Flockerzi, V.; marabashi, H.; Hiose, R.: Kodima, M.: Matsuo, H.; Hiose,
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Scheffauer, F.; Staudinger, R.; Koch, W.J.; Schwartz, A.;
Glossmann, H.
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59 LGGIIIPFSIIVIILGETLSVYCNLLHSNSFIRNNY-IATIY-KAIGTFLFGAAASQSLT 116
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                                                                                                                                                                                                                                                                                   A30063 #type complete
dlhydropyridine receptor - rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
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31.May-1991 #sequence_revision 31.May-1991 #text_change
06.Dec-1996
A37860
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##residues 1-1873 ##label TAN
##residues #length 1873 #molecular-weight 212027 #checksum 5776
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Y #length 2208 #molecular-weight 247817 #checksum 1915
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Calcium channels from Cyprinus carpio skeletal muscle.
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#title Primary structure of the receptor for calcium channel blockers from skeletal muscle.
#cross-references WID:87258269
#accession A30063
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Pred. No. 1.80e+00;
22; Mismatches 39;
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Local Similarity 26.5%; Pred. No. 1.80e+00;
nes 22; Conservative 22; Mismatches 33
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##residues 1-2208 ##label GRA
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                                                                                              116 avgqfsvgp-rdhiigncas 134
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##molecule_type DNA
##residues 134
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Rigault, S.; Rouyez, M.C.; Blanche, F.; Debussche, L.;
#Thibaut, D.
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13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change
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#formal_name Pseudomonas sp.
31-Jul-1992 #sequence_revision 31-Jul-1992 #text_change
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Pred. No. 3.76e+00;
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                                                       108 GAAASQSLTDIAKY-SIGR-LRP 128
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Best Local Similarity 28.3%;
Matches 26; Conservative
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##residues 134-135, M', 137-148, K', 150-154, K', 156-183, M', 185-189, M', 191-193; 202-211, K', 213-223, M', 225-230, K', 232-238, M', 240, M', 242-247, M', 249-263 ##label CA2 ##cross-references GB:MI6516 ##note the nucleotide sequence using the standard genetic code; the authors translation is
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NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - sea
urchin (Paracentrotus lividus) mitochondrion (SGC8)
#formal_name mitochondrion Paracentrotus lividus *common_name
                                                                                                                                                                                                                                                    Zardoya, R.; Meyer, A. Genetics (1996) 142:1249-1263
Genetics (1996) 142:1249-1263
Fre complete nucleotide sequence of the mitochondrial genome of the lungfish (Protopterus dolloi) supports its phylogenetic position as a close relative of land vertebrates.
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Gene (1987) 53-41-54
A novel gene order in the Paracentrotus lividus mitochondrial
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The complete nucleotide sequence, gene organization, and genetic code of the mitochondrial genome of Paracentrotus
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                        NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Protopterus dolloi mitochondrion (SGC1) #formal_name mitochondrion Protopterus dolloi 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 06-Dec-1996
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##cross-references EMBL:L42813
# #length 342 #molecular-weight 37535 #checksum 390
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Pred. No. 3.76e+00;
32; Mismatches 25; Indels
#type complete
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##residues 1-352 ##label CAN
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Best Local Similarity 25.0%;
Matches 22; Conservative
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Science (1995) 270:397-403
Science (1995) 270:397-403
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Pred. No. 3.76e+00;
22; Mismatches 26; Indels 10; Gaps
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08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
33-Feb-1996
S54809
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Mycoplasma genitalium (SGC3)
#formal_name Mycoplasma genitalium
17.Nov-1995 #sequence_revision 17.Nov-1995 #text_change
E64209
                                                                         *superfamily NADH dehydrogenase (ubiquinone) chain 2 membrane-associated complex; mitochondrion; NAD;
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*length 368 *molecular-weight 42083 *checksum 6298
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*length 352 *molecular-weight 39009 *checksum 8650
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Submitted to the EMBL Data Library, May 1995
S54809
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Best Local Similarity 32.6%;
Matches 28; Conservative
                                     mitochondrion
SGC8
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                                                        #genetic_code
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Nov 4 10:16:22 1997; MasPar time 7.79 Seconds 773.169 Million cell updates/sec Tabular output not generated. Run on:

>US-08-842-827-2 (1-284) from US08842827.pep 2125 1 MFDKTRLPYVALDVLCVLLA......HITLHETPTTGNHYPSNHQP 284 Description: Perfect Score: Sequence:

59021 seqs, 21210388 residues PAM 150 Gap 11 Searched:

Scoring table:

Post-processing:

Minimum Match 0% Listing first 45 summaries

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Database:

Mean 47.863; Variance 91.115; scale 0.525 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		e p			SUMMAKIES		
Result No.	Score	Query	Length	DB	Ω	Description	Pred. No.
-1	443	20.8	341	17	XSX3_CAEEL	HYPOTHETICAL 39.0 KD	8.02e-64
7	121	5.7	345	7	NU2M XENLA	NADE-UBIQUINONE OXIDO	8.14e-04
m	105	4.9	345	1	YDE9_SCHPO	PUTATIVE MITOCHONDRIA	1.30e-01
4	103	4.8	370	e	DHMH THIVE	METHYLAMINE DEHYDROGE	2.36e-01
ഗ	102	8.4	1852	~	CIC1_CYPCA	DIHYDROPRYRIDINE-SENS	3.18e-01
ø	102	4.8	1873	~	CIC1_RABIT	DIHYDROPRYRIDINE-SENS	3.18e-01
7	100	4.7	261	Ξ	YCB9_PSEDE	HYPOTHETICAL 27.4 KD	5.72e-01
œ	66	4.7	352	7	NU2M_PARLI	NADH-UBIQUINONE OXIDO	7.65e-01
6	66	4.7	382	9	LGT_MYCGE	PUTATIVE PROLIPOPROTE	7.65e-01
10	100	4.7	3388	7	POLG_DEN2P	GENOME POLYPROTEIN (C	5.72e-01
11	86	4.6	346	Ξ	YOCL_BACSU	HYPOTHETICAL 38.3 KD	1.02e+00
12	97	4.6	346	ø	NU2M_CHICK	NADH-UBIQUINONE OXIDO	1.36e+00
13	46	4.6	443	ø	MDM1_YEAST	STRUCTURAL PROTEIN MD	1.36e+00
14	86	4.6	676	~	CCMF_RHIME	CYTOCHROME C-TYPE BIO	1.02e+00
15	86	4.6	704	7	PMA2_LYCES	PLASMA MEMBRANE ATPAS	1.02e+00
16	97	4.6	723	7	CADA_BACFI	PROBABLE CADMIUM-TRAN	1.36e+00
17	86	4.6	3391	^	POLG_DEN27	GENOME POLYPROTEIN (C	1.02e+00
18	96	4.6	3391	7	POLG_DEN26	GENOME POLYPROTEIN (C	1.02e+00
19	97	4.6	3391	_	POLG_DEN2N	GENOME POLYPROTEIN (C	1.36e+00
20	95	4.5	327	σ	SYFA_ECOLI	PHENYLALANYL-TRNA SYN	2.39e+00
21	95	4.5	346	φ	NUZM_COLJA	NADH-UBIQUINONE OXIDO	2.39e+00
22	96	4.5	347	^	NU2M PHOVI	NADH-UBIOUINONE OXIDO	1.80e+00

52 grgffcdddsiryeyrkdtitavqlmlynlvlnaatvlfveyyrmqkvesni-nnpryrw 110

35 QRGVFCNDESIRYPYKEDTI-PYAL-LGGIIIPFSIIVIILGETL-SVYCNLLHSNSFI-

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NADH-UBIQUINONE OXIDO P2X PURINOCEPTOR 3 (A SODIUM-DEPENDENT NORA PROBABLE CADMIUM-TRAN HALORHODOPSIN PRECURS (CELL FUSION PROTHERIN PROBABLE CADMIUM-TRAN PROBABLE CADMIUM-TRAN PROBASMA MEMBRANE ATPAS INTEGRIN ALPHA-6 PRECIMMUNITY PROTEIN FOR RIBONUCLEOSIDE-DIPHOS PROPEIN (P45). RALPHA-1C ADRENERGIC RITTO HOST RANGE (LA MAJOR BIANDING PRO HYPOTHETICAL 9.7 KD PHYPOTHETICAL 9.7 KD PHYPOTHETICAL 9.7 KD PHYPOTHETICAL 39.3 KD ARABINOSE-PROTON SYMP SERINE HYDROXYMETHYLT HYPOTHETICAL 61.2 KD NATURAL RESISTANCE-AS	OSOME II. CERNENTEA; ROTEIN (PO	11; Length 341; -64; 80; Indels 12
NUZM_HALGR PZX3_RAT NTNO_BOVIN CADA_STAAU BACH_HALSP CELF_VZVD YBBB_STRAU ITAG_HUMAN ITA	T. 1	Score 443; Pred. No. 61; Misma
347 7 7 397 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ALIGN STANDARD; PR L. 34, CREATED) L. 34, LAST SEQUE L. 34, LAST SEQUE ELEGANS. ZOA; ACOELOMATES; A. N2; N2; N2; N2; A. N3; A. N	20.8%; larity 34.1%; Conservative
त्वच्चच्चच्चच्चचचचचचचचचचचचचचचचच १.६६६६६६६६६६६६६६६६६६६६	1 2CAEEL ST; CT-1996 (REL. CT-	h Similarity 79; Conser
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59 lghslgaf-vilavaghsgsdf-ala-stsfarsamgkrtdysgaleastfgasadnsaa 115
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-1- SUBUNIT: TETRAMER OF TWO LIGHT AND TWO HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE: 91197438.
VELLIEUX F.M.D., KALK K.H., HOL W.G.J.;
ACTA CRYSTALLOGR. B 46:806823(1990).
-!- FUNCTION: METHYLAMINE DEHYDROGENASE CARRIES OUT THE OXIDATION OF METHYLAMINE. ELECTRONS ARE PASSED FROM METHYLAMINE DEHYDROGENASE TO AMICYANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: PERIPLASMIC.
-i- CAUTION: THIS IS AN X-RAY DETERNINED SEQUENCE WHICH WAS ESTABLISHED ON THE BASIS OF THE ELECTRON DENSITY DUE TO THE LACK OF AN AMINO ACID SEQUENCE.
                                                                                                                                                                                                                                                                                                          PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC CHEMOLITHOTROPHIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CICL_CYPCA STANDARD; PRT; 1852 AA.

G12316; 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-AUG-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-CCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DIHYDROPRYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA-1 SUBUNIT.
CYPRINUS CARPTO (COMMON CARP).
EUKARYOTA, METAZOA, CHORDAIA, VERTEBRAIA, PISCES, GNATHOSTOMATA,
OSTEICHTRIES, ACTINOPPERYGII, CYPRINIFORMES.
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 90005420.
VELLIEUX F.M.D., HUITERA F., GROENDLJK H., KALK K.H., JZN J.F., JONGEJAN J.A., DUINE J.A., PETRATOS K., DRENTH J., HOL W.G.J.; BENGO J. 8:2171-2178(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A44545; A44545.
PDB; 2MAD; 31-JAN-94.
PDB; 1MAE; 31-JAN-94.
OXIDOREDUCTASE; ELECTRON TRANSPORT; PERIPLASMIC; 3D-STRUCTURE.
DISULEID 52 55
                                                                                                                                                                                                           01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
METHYLAMINE DEHYDROGENASE HEAVY CHAIN (EC 1.4.99.3) (MADH).
THIOBACILLUS VERSUTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 103; DB 3; Length 370;
Pred. No. 2.36e-01;
18; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 AA; 35778 MW; E9B4A718 CRC32;
                                                                                                                                                                       370 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS)
                                                                                                                                                                           PRT;
                                                       169 csaslgeiaacivrvptevikg 190
                                                                                             141 INCSDGYIEYYICRGNAERVKE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 DIAKYSIGRLRPHFLDVCDP 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.3%;
Matches 25; Conservative
                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
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DHMH_THIVE
P23006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BADCOCK K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (APR.1996) TO EMBL/GENBARK/DDBJ DATA BANKS.

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (POTENTIAL).

1- DOMAIN: COMPOSED OF THREE HOMOLGGOUS DOMAINS.

1- SOMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL: 270721; E235727,

HYDOTHETICAL PROTEIN; MITOCHONDRION: INNER MEMBRANE; REPEAT;

TRANSMEMBRANE; TRANSPORT.

21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 raieastkyfltgaaasal-llfssln-nawltgewsildltnplscatmtiaicmklg- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 RVKEGRLSFYSGHSSFSMYCMLEVALYLQARMKGDWARL-LRPTLQFGLVAVSTYVGLSR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 lqakggfvknggfhgvyrglgsilvgsapgaslf-fttyenmksrlsgsglglsdpqihm 168
                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE; 85261388
ROE B.A., MA D.-P., WILSON R.K., WONG R.F.-H.;
J. BIOL. CHEM. 260:9759-9774(1985).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
PIR; A00417; GOXL2M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 345;
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Pred. No. 1.30e-01;
28; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.7%; Score 121; DB 7; Length 345; Best Local Similarity 25.3%; Pred. No. 8.14e-04; Matches 21; Conservative 27; Mismatches 28; Indels
                                                                                  21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE MITOCHONDRIAL CARRIER PROTEIN C12B10.09.
SPACI2B10.09.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                 OXIDOREDUCTASE, NAD; UBIQUINONE; MITOCHONDRION. SEQUENCE 345 AA; 37671 MW; CCEBDB29 CRC32;
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D059679A CRC32;
                                                   345 A.A.
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POTENTIAL.
                                                                                                                                                                                    XENOPUS LAEVIS (AFRICAN CLAWED FROG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 VSDYKHHW-SDVLTGL-IQGALV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 lapf-hfwlpevlgglslttgli 129
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Best Local Similarity 28.0%;
Matches 23; Conservative
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128
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345 AA;
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                                                 NU2M_XENLA
P03894;
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YDE9_SCHPO
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                               RESULT
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                        MEDILIE, 9112606

GRABNER M., FRIEDRICH K., KNAUS H.-G., STRIESSNIG J., SCHEFFAUER F.,

STADDINGER R., TOCH W.J., SCHWARTZ A., GLOSSMANN H.;

PROC. NATL. ACAD. SCI. U.S.A. 88:727-731(1991).

-1- FUNCTION: CALCIUM CHANNEL PROFERIN WHICH PLAYS AN IMPORTANT ROLE IN

EXCITATION-CONTRACTION COUPLING. THE ALPHA-1 SUBUNIT BINDS

DIMYDROPYRIDINE (DHP), A CALCIUM CHANNEL BLOCKER.

-1- SUBURIT THIS L.TYPE CALCIUM CHANNEL IS COMPOSED OF TWO SUBUNITS:

ALPHA-1, AND ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYKEDTIPYALLGGIIIPFSIIVIILGETLSVYCNLLHSNSFIRNNYIATIYKAIGTFLF 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                     IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCOPROTEIN; DUPLICATION; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 33; Indels
                                                                                                                                                               -: - PTM: MAT NOT BE PROSPHORIZATED MICHAEL FROITENT.
-: - TISSUE SPECIFICITY: SKELETAL MUSCLE.
-: - SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS.
-- BERL: MGZ254; G213050; -
-- PTR: A37860; A37860.
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PHOSPHORYLATION (BY
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Best Local Similarity 26.5%;
Matches 22; Conservative
SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
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HUI A., SCHWARTZ A.,
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-1- SUBBUILT: THE L-TYPE CALCIUM CHANNEL BLOCKER.

-1- SUBBUILT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: SKELETAL MUSCLE.

-1- SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS.

EMBL; X05521; G1548; --

EMBL; X05521; G1548; --

FIRS, X30063; A30063;

FIRS, A30063; A30063;

CALCIUM CHANNEL; TRANSHEMBRANE; ION TRANSPORT; VOLTAGE-GATED CHANNEL;

CALCIUM CHANNEL; GLYCOPROTEIN; DUPLICATION; PHOSPHORYLATION.
                                                                                                                                                             DIHYDROPRYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANABE T., TAKESHIMA H., MIKAMI A., FLOCKERZI V., TAKAHASHI H., KANGAWA K., KOJIMA M., MATSUO H., HIROSE T., NUMA S.; NATURE 328:313-318(1987).
                                                                                                                                                                                                                              ORYCTOLAGUS CUNICULUS (RABBIT).
EUKRRYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; LAGOMORPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELLIS S.B., WILLIAMS M.E., WAYS N.R., BRENNER R., SHARP A.H., EDENG A.T., CAMPBELL K.P., MCKENNA E., KOCH W.J., HUI A., SCHARPOLD M.M.;
SCIENCE 241:1661-1664(1988).
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S2 OF REPEAT I.

S4 OF REPEAT I.

S5 OF REPEAT I.

S5 OF REPEAT II.

S1 OF REPEAT II.

S2 OF REPEAT II.

S3 OF REPEAT III.

S4 OF REPEAT III.

S5 OF REPEAT III.

S5 OF REPEAT III.

S6 OF REPEAT III.

S6 OF REPEAT III.

S7 OF REPEAT III.

S6 OF REPEAT III.

S7 OF REPEAT III.

S6 OF REPEAT IV.

S7 OF REPEAT IV.

S8 OF REPEAT IV.

S7 OF REPEAT IV.

S8 OF REPEAT IV.
                                                             07, CREATED)
07, LAST SEQUENCE UPDATE)
27, LAST ANNOTATION UPDATE)
1873 AA
   PRT;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 87258269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 88336904.
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01-APR-1988 (REL.
01-OCT-1993 (REL.
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OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION SEQUENCE 352 AA; 39009 MW; 39BB4327 CRC32;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE; 96026346.
                                                                                                                                                                                    STANDARD;
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123
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302
382 AA;
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P47332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 PYKEDTIPYALLGGIIIPF-SIIVIILGETLSVYCNLLHSNSFIRNNYIATIYKAIGTFL 106
                                                                                                                                                                                                                                                                                                                                                                                                                             4.7%; Score 100; DB 11; Length 261;
11.1%; Pred. No. 5.72e-01;
ttive 18; Mismatches 21; Indels 3; Gaps
                                                                           3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANTATORE P., ROBERTI M., RAINALDI G., GADALETA M.N., SACCONE C., J. BIOL. CHEM. 264.10965-10975(1989).
J. BIOL. CHEM. 264.10965-10975(1989).
EMBL., JOAGLIS, G453499; -.
PIR; B34284; B34284.
                                                                                                                                                                                                                         01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-ULL-1993 (REL. 26, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.4 KD PROTEIN IN COBO 3'REGION (ORF9).
PSGUDOMONAS DENTIRITICANS.
PROKRAYOTA: GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                         MEDLINE; 92011366.
MEDLINE; 92011366.
MEDLINE; 92011366.
ROUZET J., LEVY-SCHIL S., CAMERON B., CAUCHOIS L., RIGAULT ROUYEZ M.-C., BLANCHE F., DEBUSSCHE L., THIBAUT D.; J. BACTERIOL. 173:6074-6087(1991).
ENBL; MGS1866; G551929; -.
PIR.; 138164; J38164.
HYPOTHETICAL PROTEIN; MEMBRANE.
SEQUENCE 261 AA; 27374 MW; 5D508436 CRC32;
                                                       Length 1873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRION.
EURARYOTA: METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
EUECHINOIDEA.
                                                                          22; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).
 T -> M (IN REF. 2).
A -> V (IN REF. 2).
A -> E (IN REF. 2).
BA27142C CRC32;
                                                     Score 102; DB 2;
Pred. No. 3.18e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 AA
                                                                                                                                                                                                       261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARACENTROTUS LIVIDUS (COMMON SEA URCHIN).
                                                                                                                                      881 ismglesstisvvkilrvlrvlrp 904
                                                                                                                                                           107 FGAASQSLTDIAKY-SIGR-LRP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1989 (REL. 12, CREATED)
 1808 1808
1815 1815
1835 1835
1873 AA; 212028 M
                                                    4.8%;
Local Similarity 23.8%;
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 31.1%;
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                       STANDARD;
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SEQUENCE FROM N.A.
MEDLINE; 89291831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NU2M_PARLI
P12771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989
01-NOV-1990
                                                                                                                                                                                                     YCB9_PSEDE
P29942;
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CONFLICT
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SEQUENCE
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P12833;
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GENOME POLIPROTEIN (CONTAINS: CAPSID PROPERT C
FOURTH POLYBEOTEIN (STANDARD SOLFEN E)
NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRASER C.M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,
FLEISCHMANN R.D., BULT C.J., KERLAVAGE A.R., SUTTON G., KELLEY J.M.,
EFLISCHMANN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRMANN J.L.,
NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIES C.A., MERRICK J.M.,
TOMB J.-F., DOUGHERIYY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,
SCIENCE 270:397-403(1995).
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)
PUTATIVE PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE (EC 2.4.99.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYCOPLASMA GENITALIUM.
PROKARYOTA; TENERICUTES; MOLLICUTES; MYCOPLASMA; MYCOPLASMATALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: TRANSFERS THE N-ACYL DIGLYCERIDE GROUP ON WHAT WILL BECOME THE N-TERMINAL CYSTEINE OF MEMBRANE LIPOPROTEINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
--- SUBCELLCLEAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
---- PATHWAY: FIRST STEP IN LIPOPROTEINS BIOSYNTHESIS.
EMBL; U39688; G1045763; --
                                                   26; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99; DB 6; Length 382;
Pred. No. 7.65e-01;
13; Mismatches 18; Indels
  Length 352;
Score 99; DB 7; L. Pred. No. 7.65e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
5D374E0F CRC32;
                                                                                                                                                                                                                                                                                                                                                          382 AA.
                                                 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                          PRT;
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Query Match
Best Local Similarity 32.6%;
Matches 28; Conservative
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Best Local Similarity 34.7%;
Matches 17; Conservative
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32, CREATED) 32, LAST SEQUENCE UPDATE) 34, LAST ANNOTATION UPDATE)

346 AA

PRT;

STANDARD;

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PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-168 / JH642;
KOBAYASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S., SATO T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 96084975.
MEDIGUE C., MOSZER I., VIARI A., DANCHIN A.;
GENE 165:GC37-GC51(1995).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
SERAIN-168 / JH642;
MEDLINE: 95219086.
TAKEMARU K.-I., MIZUNO M., SATO I., TAKEUCHI M., KOBAYASHI '
                                                                                                                                                                                        01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 38.3 KD PROTEIN IN CWLA-CISA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBTILIST; BG11303; YQCL.
HYPOTHETICAL PROTEIN; TRP
TRANSMEM 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D32216; G1217884;
EMBL; D84432; G130377;
                                                                                                                                                                                                                                               BACILLUS SUBTILIS
                                                                                                                                                   01-NOV-1995 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION
       1362 las 1364
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                                           241 LVA 243
                                                                                                                                                                      01-NOV-1995
                                                                                                                 YOCL_BACSU
P45946;
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TRANSMEM
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NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
-i- SUBDAIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN G AND MANA.

EMBL. M19197; G323655;
POLYFROTEIN G AND MANA.
PIR. A29972; GNWYDP.
POLYPROTEIN: GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; OUNSTRUCTURAL PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE;
                                                                                            SEQUENCE FROM N.A.
MEDLINE; 88101365.
HARN Y.S., GALLER R., HUNKAPILLER T., DALRYMPLE J.M., STRAUSS J.H.
STRAUSS E.G.;
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5)).
DENGUE VIRUS TYPE 2 (STRAIN PR159/S1).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
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Pred. No. 5.72e-01;
20; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONSTRUCTURAL PROTEIN NSI-
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
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DEAH BOX.
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WEDLINE; 99294842
WRICHT P. J., CAUCHI M.R., NG M.L.;
VIROLOGY 171:61-67(1989).
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Local Similarity 30.2%;
nes 19; Conservative
                                                                                                                                                                                                        C-TERMINAL OF M, E, AND NS1
                                                                                                                                                                  VIROLOGY 162:167-180(1988)
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                                                          FLAVIVIRUSES
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01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 98; DB 11; 1
Pred. No. 1.02e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               larity 23.7%;
Conservative
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61
102
102
1160
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318
346 AA;
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tes 14; Conser
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SEQUENCE FROM N.A.
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CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK
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PROSITE; PS00154; ATPASE_E1_E2
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Best Local Similarity 35.3%;
Matches 18; Conservative
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                                                                                                           RHIZOBIACEAE.
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SELTON J., CHURCHER C.M., BARRELL B., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (MAY-1955) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ESSENTIAL FOR MITOTIC GROWTH. MEDIATE ORGANELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: LOW, TO VIMENTIN AND OTHER INTERMEDIATE FILAMENTS.
EMBL: X65371; 63916; -.
EMBL: 249210; 6798896; -.
PIR; A42636; A42636.
-151STA; SCO0593; MDM1.
SGD: LOO1051; MDM1.
CONFLICT 88 88 Q -> R (IN REF. 1).
                 DESJARDINS P., MORAIS R.;
J. MOL. BIOL. 212:599-634(1990).
J. MOL. BIOL. 212:599-634(1990).
EMBL. X52392; G12962.
PIR; S10108. S10184.
SI0108. S10184.
SEQUENCE 346 AA; 38333 MW; 60A7C67B CRC32;
                                                                                                                                                                                                                                Score 97; DB 6; Length 346;
Pred. No. 1.36e+00;
33; Mismatches 28; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDMI OR YML104C OR YM8339.15C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKRAROTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Le
1.36e+00;
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32, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
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(REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCCONNELL S.J., YAFFE M.P.;
J. CELL BIOL. 118:385-395(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (REL. 27, CREATED)
01-FEB-1996 (REL. 33, LAST SEQ
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Local Similarity 26.0%;
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Local Similarity 34.4%;
les 11; Conservative
                                                                                                                                                                                                                                                                                           25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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MEDLINE; 92332595.
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MEDLINE; 90230301
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215
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P45404;
01-NOV-1995 (
01-NOV-1995 (
01-NOV-1995 (
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AC 001846;
DT 01-0CT-1993
DT 01-FEB-1996
DT 01-FEB-1996
DE STRUCTURAL F
GN MADAL ON YALL
OS SACCHAROWYCE
RN [1] RAP SEQUENCE FRK
RN MEDLINE; 92:
RA MCCONNELL S
RL J. CELL BIOJ
RP SEQUENCE FRK
RC STRAIN=S2888
RC S
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ID CC
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-:- CATALYTIC ACTIVITY: ATP + H(2)O - ADP + ORTHOPHOSPHATE.
-:- SUBUNIT: POSSIBLY EXISTS AS AN HOWODIMER OR AN HOMOTRIMER.
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- AS MANY AS 6 TO 8 CLOSELY RELATED GENES MAY ENCODE OTHER ISOFORMS OF PLASAN MEMBRANE ATPASE IN TOWARO, LIKE THE LHAI GENE PRODUCT WHICH IS 96% IDENTICAL TO THE LHAZ GENE PRODUCT.
-:- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                  KERESZT A., SLASKA-KISS K., PUTNOKY P., BANFALVI Z., KONDOROSI A.;
SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: REQUIRED FOR THE BIOGENESIS OF C-TYPE CYTOCHROMES.
POSSIBLE SUBUNIT OF A HEME LYASE.
-!- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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HENGELS, MEYER D.J., CHETELAT R.T., BENNETT A.B.;
PLANT PHYSIOL.
PLANT PHYSIOL.
-!- FUNCTION: THE PLASMA MEMBRANE ATPASE OF PLANTS AND FUNGI IS A
HYDROGEN ION PUMP. THE PROTON GRADIET IT GENERATES PRYVES THE
ACTIVE TRANSPORT OF UNTRIENTS BY H+- SYMPORT. THE RESULTING
EXTERNAL ACIDIFICATION AND/OR INTERNAL ALKINIZATION MAY MEDIATE
RHIZOBIUM MELILOTI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMA2_LYCES STANDARD; PRT; 704 AA. P238B0; 01-NOV-1991 (REL. 20, CREATED) 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE) 01-NOV-1991 (REL. 33, LAST ANNOTATION UPDATE) PLAŞMA MEMBRANE ATPASE 2 (EC 3.6.1.35) (PROTON PUMP) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/YCF5 FAMILY.
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EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 lylgyvgfsv-cfsfavaaliegridaawarwvrpwtlaawtfltagiamg 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X82560; G575372; -- CTTOCHROME C-TYPE BIOGENESIS; TRANSMEMBRANE; INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 98; DB 2; Length 676;
Pred. No. 1.02e+00;
14; Mismatches 15; Indels
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C9947521 CRC32;
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Query Match
4.6%; Score 98; DB 7; Length 704;
Best Local Similarity 27.4%; Pred. No. 1.02e+00;
Matches 23; Conservative 19; Mismatches 38; Indels 4; Gaps
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Search completed: Tue Nov 4 10:17:09 1997 Job time: 47 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm л. а. MPsrch_nn MasPar time 1306.58 Seconds 1316.341 Million cell updates/sec 6 10:42:02 1997; Thu Nov 00

Tabular output not generated.

>US-08-842-827-3 (1-1565) from US08842827.seq 1566 Description: Perfect Score: N.A. Sequence:

TABLE default Scoring table:

Gap 6

Dbase 0; Query 0

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STD

Nmatch

362067 segs, 549138275 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-new3 Database

1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC

genbank99

Database

18. BCT 1 19. BCT 2 20. BCT 3 21. BCT 4 22. BCT 5 23. BCT 6 24. BCT 7 25. BCT 3 25. BCT 2 27. BCT 1 29. GENT 3 00. GENT 3 25. BCT 3 25. BCT 1 2 29. GENT 3 00. GENT 3 31. BCT 3 24. BCT 1 2 29. GENT 3 00. GENT 3 38. INV 4 39. INV 5 37. INV 3 38. INV 4 39. INV 5 37. INV 3 38. INV 4 39. INV 5 40. INV 6 41. INV 7 4 21. INV 8 43. INV 9 44. INV 10 55. INV 7 45. INV 1 46. INAM 1 46. INAM 1 48. INAM 2 49. INV 1 50. VRT 5 1. VRT 5 3. PRT 1 54. PAT 5 55. PAT 3 56. PAT 4 57. PAT 5 8. PRG 59. PLN 6 60. PLN 6 61. PLN 6 62. PLN 6 63. PLN 6 63. PLN 6 63. PLN 6 65. PLN 7 77. PRT 1 88. FROD 8 87. ROD 8 97. ROD 9 97. VRL 9 98. VRL 9 99. VRL 4 100. VRL 5 101. VRL 6 102. VRL 7 103. VRL 8 104. VRL 9

genbank-new3 105:VRL10

106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2 118:ROD 119:SYN 120:UNA 121:VRL

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 11.944; Variance 6.199; scale 1.927

1212 bp mRNA ROD 03-OCT-1996 Musculus domesticus kidney mRNA for Phosphatidic acid complete cds. 0.00e+00 4.06e+178 7.06e+57 1.76e-57 2.48e-51 2.48e-04 4.31e-04 1.39e-02 1.39e-02 1.39e-02 4.73e-01 1.57e-01 5.09e-01 1.61e+00 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Piromyces sp. mRNA fo 4.
C.aureus GNAT2 gene 1.
R.norvegicus mRNA for 5.
D.obscura AT-rich re 5.
Mouse Muril mRNA, exo 5
Mouse Muril mRNA, exo 5 Plasmodium falciparum 5.

Human DNA sequence ** 5.

O.sativa mRNA for T23 1.

Brassica napus antifu 1. Phosphatidic acid phosphatase; 35-kDa phosphatidic acid Sequence 5 from paten Sequence 5 from paten S.solidissima mRNA fo Drosophila melanogast Bombyx mori fibroin 1 Drosophila melanogast.
Dictyostelium discoie
B.taurus mRNA for cyc
R.norvegicus P2X mRNA Mouse Murri mRNA, exo L.polyphemus mRNA for Dictyostelium discoid Zw-glucose-6-phosphat Plasmodium chabaudi d Plasmodium falciparum R.norvegicus mRNA for Dictyoselium discoide Yeast cytochrome c ox Dictyostelium discoid Myrmecia pilosula HI8 C.tentans mRNA for hr Plasmodium falciparum H. sapiens mRNA for Ar Dictyostellum discoid Panulirus argus gluta Hydra magnipapillata D.discoldeum gp80 gen Plasmodium falciparum Plasmodium falciparum R.norvegicus mRNA for Human clone 23748 mRN Human mRNA for KIAA00 Description Mus musculus kidney cDNA to mRNA. Mus musculus ALIGNMENTS HUMORFA02 RNDR142 HSU79294 128278 128278 SSM2RR SM2RR BM0111584 BM0111565 DM037541 HS435C23 A23327 BNU59459 SCCOX1 DDICSA MPU15677 CTHRP45MR HSARGBPIA DDU53884 DD19 S67872 PCU53325 PFU07706 HS435C23 RNA7CINT DOATRICH PFAHGPTA PNLGTSYN BBCA RNP2XMR PSMANC RNIAC DDICNPA PFARPI MMD430 D85430 CAGNAT2 MMD430 LPACT3 110 122 54 61 DB 39 43 2049 Length House mouse; phosphatase, phosphatase. Query 91487872 Score DEFINITION ORGANISM ACCESSION KEYWORDS Ņ. Result

(bases 1 to 1212)

REFERENCE AUTHORS TITLE

Direct Submission
Submitted (10-APR-1996) to the DDBJ/EMBL/GenBank databases. Hideo
Submitted (10-APR-1996) to the DDBJ/EMBL/GenBank databases. Hideo
Kanch, Sapporo Medical University School of Medicine, Department of
Biochemistry, West-17, South-1, Sapporo, Hokkaido 060, Japan
(E-mail:Kanch@serpent.cc.sapmed.ac.jp, Tel:011-611-2111(ex.2290),
Fax:011-612-5861) Kanoh, H.

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Pred. No. 4.61e-178;
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/tissue_type="calvariagag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="HIC-53"
/cell_line="MC3T3-E1"
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                                                                                                                                                                                      /product-"Phosphatidic acid phosphatase"
/db_xref="PiD:g1487873"
/db_xref="PiD:g1487873"
/translation-"MEDKTREPVVALDVICVLLAGLPFAILTSRHTPFORGIFCNDDS
IKYFYKEDTIPYALLGGIVIPFCIIVMSIGESLSVYFNVLHSNSFVGNPTIATIYKAV
GAFLEPVSAAGSLTDIAKTIGGIRPHTLAICNPDKSKINCSDGYIEDYICOGREEKV
KEGRLSFYGGHSSFSWYCMLFVALVLOARWKGDWARLLRFWLOFGLIAFSIYVGLSRY
SDTXHHWSDVTVGLIGGAAWAILVALYVSDFFKDTHSYKERKEEDPHTTHEFASSRN
        Kal, W. Wade, T., Imal, S., Sakane, F. and Kanoh, H. Identification and cDNA cloning of 35-Kb phosphatidic acid phosphatase (type 2) bound to plasma membranes. Polymerase chain reaction amplification of mouse H202-inducible hic53 clone yielded the cDNA encoding phosphatidic acid phosphatase 9334980.
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                                                                                                                         /organism="Mus musculus"
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/evidence-experimental
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/product="hydrogen peroxide-inducible protein"
/db_xref="PID:g1161100"
/db_xre Isolation of a novel ras-recision gene that is induced by hydrogen peroxide from a mouse osteoblastic cell line, MC3T3-E1 96032549 'n Muridae; MUSHDIP 1490 bp mRNA ROD 11-JAN-1996 Mus musculus (clone HIC-53) hydrogen peroxide-inducible protein mRNA, complete cds. 438 gogaggaatattetgtaatgatgactecateaagtaceettacaaggaagacaceatace 497 508 557 321 ccagccggtgaccatgttcgacaagacgcggctgccgtacgtggccctcgatgtgatttg 380 381 cgtgttgctggctggattgccttttgcaattcttacttcaaggca--taccccc-ttcca 437 Gaps CDNA to mRNA agotgotataggotatactggttgctttgtatgtatccgatttcttcaaggacacacttc 449 GAGAGGCTTTTTCTGTAAAGACAACAGCATCAACTATCCGTACCATGACAGTACCGCCGC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; gli61099 hydrogen peroxide; hydrogen peroxide-inducible protein. Mus musculus Mus musculus 5, Length 1490; 1051 ttacaaagaagaaaggaaggatccacacacgectctccatgaaac 1098 0; Mismatches 139; Indels Murinae; Mus. 1 (bases 1 to 1490) Egawa, K., Yoshiwara, M., Shibanuma, M., and Nose, K.

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Seki,N., Kawarabayasi,Y., Ishikawa,K. and Tabata. Sa.A.
Prediction of the coding sequences of unidentified human genes. II.
The coding sequences of 40 new genes (KIAA0041-KKAA0080) deduced by
analysis of cDNA clones from human cell line KG-1
96051398
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Submitted (22-MAR-1994) to the DDBJ/EMBL/GenBank databases.
Nobuyuki Miyajima, Kazusa DNA Research Institute, Laboratory of Genome Information; 1532-3 Yanauchino, Kisarazu, Chiba 292, Japan (E-mail:miyajima@kazusa.or.jp, Tel:0438-52-3917, Fax:0438-52-3918)
509 ATCCACTGTCCTCATCCTAGTGGGGGTTGGCTTGCCCGTTTCCTCTATTATTCTTGGAGA 568
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1 (bases 1 to 3353)
Miyajima,N.
                                                                                                           558 atctctgtctgtttactttaatgtcttgcattcgaattcctttgtcggcaatccctacat
                                                                                                                                                                                                                                                             738 cccagactggtcaaaaatcaactgcagtgatggctatattgaggactacatatgtcaagg
                                                                        569 AACCCTGTCTGTTACTGTAACCTTTTGCACTCAAATTCCTTTATCAGTAATAACTACAT
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Homo sapiens
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Human mRNA for KIAAO052 gene, partial cds
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/cell_line="KG-1"
/cell_type="myeloblast"
/sex="male"
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Kisarazu, Chiba 292
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LPDNVHYYPTSAGT TDNAKQFAEWICHLAKQCHVIYTDYRPTPLQHYITERGKOBGLH
VVDENGDFREDNFNTAMOVLRDAGDLAKGDQKGRKGGTKGPSNVFKIVKMIMERNFOP
VITESFRKKLOEAYALQYKLLDFNDERKWYMEEVESNAICLSDEBEKTLDVGEBTVLF
LLKRGIGTHRGGLIDILKETIEILFSEGLIKALFAPETFAMGINNPARTVLFYRARKE
DGKDFRWISSGEYIQMSGRAGRRGMDDRGIVILMVDEKMSPTIGKOLLKGSADPLNSA
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SAISSVRLYIPKDLRPVDNROSVLKSIQEVOKRFPDGIPLLDPIDDMGIQDQGLKKVI
QKVBAFEHRMYSHPLHNDPNLETVYTLCEKKSTDCNRY"
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ESVVIYYKIRQQLAKLGKEIEEFIHKPKYCLPFLQPGRLVKVKNEGBDDFGWGVVVNFS
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Barila,D., Plateroti,M., Nobili,F., Muda,A.O., Xie,Y., Morimoto,T.
and Perozzi,G.
The Dri 42 gene, whose expression is up-regulated during epithelial
differentiation, encodes a novel endoplasmic reticulum resident
/db_xref="PID:g473933"
/translation="LLPRMADAFGDELFSVFEGDSTTAAGTKKDKEKDKGKWKGPPGS
                                                     ADKACKRFDGKLOSESTNNGKNKRDVDFEGTDEPIFGKKPRIEESITEDLSLADLMPR
VKVQSVETVEGCTHEVALPAEEDYLPLKPRVGKAAKEYPFILDAFQREAIQCVDNNQS
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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0; Mismatches 0; Indels
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R.norvegicus mRNA for ER transmembrane protein.
Y07783
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J. Biol. Chem. 271 (47), 29928-29936 (1996)
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Dri 42 gene; ER-transmembrane protein.
Norway rat.
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/dev_stage="adult"
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Perozzi, G.
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1 560 c
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Best Local Similarity 100.0%;
Matches 130; Conservative
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FMAGLPFLIIETSTIKPYHRGFYCNDESIKYPLKTGFTINDAVLCAVGTVIAILATIT
GEFYRIYLKKSRSTIONPYVAALYKOVGCFLFGCAISOSTDIAKVSIGRLRPHFLS
VCNPDFSOINCSEGYTONYRCRGDDSKVQEARKSFFSGHASFSMYTMLYLVLYLQARF
TWRGARCSGSSGSSF
                                                                                                      /product="unknown"
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/translation="MQNYKYDKAIVPESKNGGSPALNNNPRRSGSKRVLLICLDLFCL
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375..107
                                                                                                                                                                                                            317
                    /sex="female"
/dev_stage="infant"
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8 c 25 g
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Local Similarity 62.8%;
nes 263; Conservative
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1444)
Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A. A'double adaptor' method for improved shotgun library construction A. Anal. Blochem. 236 (1), 107-113 (1996)
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8930, Houston, TX 77030, USA
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                                                                                                                                                                                                                                   830 agccagtcetteacagacategecaaagtgtecattgggegeetgaggeeteaetteete 889
                                                                                                                                                                                                                                                                                          890 agcytctgtgaccctgatttcagtcagatcaattgctccgagggctacattcagaactac 949
                                                                                                                                                                                                                                                                                                           GGAGACTGGGCAAGACTCTTACGCCCCACACTGCGATTTGGTCTTGTTGCCGTATCCATT 977
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Ricefrence,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
Tyrep Scale Concatenation cDNA Sequencing
Unpublished
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                                                                                                                                                                           Score 111; DB 91; Length 2206;
Pred. No. 1.76e-57;
0; Mismatches 136; Indels 0
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Human clone 23748 mRNA, complete cds.
U79294
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1 Similarity 64.5%;
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tacacgggactgtctcgcgtatcagaccacaagcaccatcccagtgatgttctggcagga 1150
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Bennett.A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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      Length 1444;
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Score 102; DB 78; Length 144
Pred. No. 9.39e-51;
0; Mismatches 155; Indels
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Pred. No. 2.48e-08;
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128278
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Best Local Similarity 17.1%;
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Matches

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RESULT

DEFINITION

ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE

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/product="MX" (small) subunit of ribonucleotide reductase"
/db_xref="PID:q10342"
/db_xref="SHIS:4D0342"
/db_xref="SHIS:4D0342"
/db_xref="MLSINTFRENELSGNIGKMKITEENKPKKVLGEIINFORSTOK
TPLKQEIKPVVKKSQQVEPLLADNPRRFVVLPIQYHDIWKWYKRAEASFWTAEEVDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDMAHWESLKKEEKHFISHVLAFFAASDGIVNENLVERFSKEVQVTEARCFYGFQIAM
ENIHSEMYSLLIDTYIKDPQERDFLFNAIETWPCVKEKADWAMRWINDDSSSYAERVV
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KENPFDFMEHISLEGKTNFFEKRVGEYQKMGVMSGGNTGDSHAFTLDADF"
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1 (bases 1 to 4601)

1 (ewis, D.L., Farr, C.L., Farquhar, A.L. and Kaguni, L.S. Sequence, Organization and Evolution of the A+T Region of Drosophila melanogaster Mitochondrial DNA

Mol. Biol. Evol. 11, 523-538 (1994)
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/note="mescription: mitochondrial origin; repeat I-A"
/rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (03-NOV-1990) Hunt T., Standart N., Department of
Submitted (03-NOV-1990) Hunt T., Standart N., Department of
1 chases 1 to 1727)
Standart,N., Dale,M., Stewart,E. and Hunt,T.
Genes Dev. 4 (1990) In press
Forms a complex with the product of the large MI subunit of
ribonucleotide reductase.
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Blochemistry, Michigan State University, East Lansing, MI,
48824-1318, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DMU11594 4601 bp DNA 13-JUL-1
Drosophila melanogaster Oregon-R mitochondrial A+T region
U11584
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Pred. No. 4.01e-03;
0; Mismatches 13; Indels
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fruit fly.
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                                                                                                                                                                                                                                 /organism="Spisula solidissima"
/dev_stage="ocoyte"
/cell_type="ocoyte"
96..1250
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                                                                                                                                                                                                                                                                                                                       /EC_number="1.17.4.1"
                                                                                                                                                                                          Location/Qualifiers
1..1727
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/dev_stage="embryo"
650..1022
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    Hunt, T. and Standart, N.
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Best Local Similarity 77.6%;
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Spisula solidissima
Eukaryotes, mitochondrial eukaryotes; Metazoa; Mollusca; Bivalvia;
Heteroconchia; Veneroida; Mactridae; Spisula.
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                                                             Tobases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                                                                                                        71 nnvgaakthyythtnvsgadsktvtdsynasgtsssnggtdgnr-sgadsygssktamts 129
                                                                                                                                                                                                          130 rnrtgktannavdsrnmgdasvgsdkntkkhakns-adgkvgsknngdrnnrygtgtksn 188
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S.solidissima mRNA for M2 (small) subunit of ribonucleotide
reductase.
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Pred. No. 3.13e-04;
88; Mismatches 95; Indels
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Sequence 5 from patent US 5569830.
128278
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Best Local Similarity 11.5%;
Matches 24; Conservative
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                                                                                                                                            Eukaryotae: mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata: Insecta; Pterygota; Lepidoptera; Bombycoidea; Bombycidae; Bombycidae; Lo 14626) Kichoses in to 14626) Kikuchi,Y., Mori,K., Suzuki,S., Yamaguchi,K. and Mizuno,S. Structure of the Bombyx mori fibroin light-chain-encoding gene: upstream sequence elements common to the light and heavy chain 92165053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(1028..1104.9250..9332,10532..10727,11412..11555,
12196..12284,13361..13505,14061..14499)
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                                                                                                 Élbroin light chain.
Bombyx mori 5th instar larvae posterior silk gland DNA.
Bombyx mori
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Matches 78; Conservative 0; Mismatches 41; Indels 1;
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                                                                                                                                                                                              Evolution of Drosophila mitochondrial DNA and the history of the melanogaster subgroup
Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9558-9562 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster mitochondrial DNA: gene organization and
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db_xref="FlyBase:EBgn0013685"
/product="tRNA-f-met (CAO)"
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/note-"Description: mitochondrial NADH-ubiquinone
oxidoreductase chain 6
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/mitochondrion
/note="derived from new and previously submitted
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/db_xref=FlyBase:FBgn0013685"
/db_xref=FlyBase:FBgn0013685"
/product="NADH dehydrogenase subunit 2"
/db_xref="PlD:g1166530"
/transl_table=5
Drosophila melanogaster and its sibling species Mal. Biol. Evol. 4 (6), 638-650 (1987)
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/product-"tRNA-lle (GAU)"
complement(97.165)
/gene-"mt:ND6"
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Lewis, D.L., Farr, C.L. and Kaguni, L.S.
Direct Submission
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171..239
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Genetics 118 (4), 649-663 (1988)
88212147
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                                                                                                                                                            Satta, Y. and Takahata, N.
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Transfer RNA genes in Drosophila mitochondrial DNA: related 5'
flanking sequences and comparisons to mammalian mitochondrial tRNA
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Insecta; Pterryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilae; Drosophila.

[ kases 1 to 408; 13319 to 19517)
Ewwis, D.L., Farr, C.L. and Raguni, L.S.
Drosophila melanogaster mitochondrial DNA: completion of the nucleotide sequence and evolutionary comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-1996
complete sequence.
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Satta,Y., Ishiwa,H. and Chigusa,S.I.
Analysis of nucleotide substitutions of mitochondrial DNAs in
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Molstenholme, D.R.

Drosophila mitochondrial DNA: a novel gene order

Nucleic Acids Res. 10 (21), 6619-6637 (1982)
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0; Mismatches 26; Indels
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Drosophila melanogaster mitochondrial genome,
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/gene="Fib-L"
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de Bruijn, M.H.
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/gene="Fib-L"
13506..14060
/gene="Fib-L"
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2726 c 2
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Local Similarity 70.0%;
hes 63; Conservative
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AGSADSTVSLWDIEDDMCVKTFIKSTFPCRSVSFSPDGGFIAASSFESTIEIFHIESS
QPIHTIECSGVSSLMWHPTLPLLAYAPEINENNKDPSIRVFGYHS
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Shaw,D.R., Richter,H., Glorda,R., Ohmachi,T. and Ennis,H.L.
Nucleotide sequences of Dictyostelium discoideum developmentally
regulated cDNAs rich in (AAC) imply proteins that contain clusters
of asparagine, glutamine, or threonine
Mol. Genet. 218 (3), 453-459 (1989)
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/note="Description: mitochondrial NADH-ubiquinone
                                                                                                                                        /note-"Description: mitochondrial NADH-ubiquinone oxidoreductase chain 6"
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                                                                                                                                                                                                                                                            Length 19517;
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Pred. No. 4.73e-02;
0; Mismatches 11; Indels (
                                                                                                                                                                                                                                                            Score 31; DB 40; Length 1953
Pred. No. 1.39e-02;
0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostellum discoledeum AAC-rich mRNA (AAC3). x16524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Dictyostellum discoideum"/clone_lib="lambda gt10"
/clone="AAC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"coding region (AA 1 - 437)"
                                    /db_xref="FlyBase:FBgn0013685"
/product="tRNA-Asp (GUC)"
3907..4068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/db_xref="PID:97176"
/db_xref="SWISS-PROT:P14197"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="glutamine cluster"
198 c 200 g 431
                       oxidoreductase chain 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA
                                                                                                                                                                                                              Note: remainder of annotations omitted,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutamine rich protein.
Dictyostellum discoideum.
Dictyostellum discoideum
                                                                                                                 /gene="mt:ND6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1427 bp
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 65.0%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 78.8%;
Matches 41; Conservative
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="SrowlestwhedigtlyFifgawagmygtslsiliraelghpga
Ligddoirwiytahaffmiffwwpfmiggfgmyyplulgapdwaffrmnwsffwl
LippalsillySswemgagfgmyypplsagiahegasydlaifselhafisstigay
NeityVinrsyfgisldbaplffwwsyvitallilschvlagaifmliydrimtsff
DpagggdpilxQhlffwffghpevyIlllpgfgmishiisgesgkkeffgslgmiyaml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIGLIGETUWAHHMETVGMDVDTRAYETSATMIIAVPTGIKIFSWLATLHGTQLSYSP
ATLMALGEVELEVYGGLTGVVLANGSYDIILHDTYYVVAHFHYVLSMGATBAIMAGET
HWYPLFTGLTLENKKLKSHFILMFICVNLFEPQHFLGLAGWPRRYSDYPDATTTWNI
VSTIGSTISLLGILFFFPIIWESLVSQRQYIYPJQLNSSIEWYQMTPPABHSYSELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFFNNYVNRFLLHGQLIEMIWTILPAIILLFTALPSLRLLYLLDEINEPSYTLKSIGH
QWYWSYEYSDSFNNIEFDSYMIPTNELMTDGFRLLDVDNRVVLPMNSQIRILVTAADVI
HSWTVPALGVKVDGTPGRLNQTNFFINRPGLFYGQCSEICGANHSFMPIVIESVPVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSTWANLGLQDSASPIMEQLIFFHDHALLILVMITVLVGYLMFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //orde="Description: mitochondrial NADH-ubiquinone oxidoreductase chain 6; incomplete stop codon, requires polyadenylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidoreductase chain 6; ATAA, putative translation initiation codon for cytochrome c oxidase subunit I* Cab_xref-"Flybase:FBgn0013685"
       1264..1329
/gene="mt:ND6"
/note="Description: mitochondrial NADH-ubiquinone
oxidoreductase chain 6"
/db.xef="FlyBase:FBgn0013685"
/product-"tRNA-Trp (UCA)"
complement[1322..1383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"mt:ND6"
/note-"Description: mitochondrial NADH-ubiquinone
                                                                                                                                                                                                                                                                                                                                                    /note="Description: mitochondrial NADH-ubiquinone oxidoreductase chain 6"
                                                                                                                                                                                                      /note-"Description: mitochondrial NADH-ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Description: mitochondrial NADH-ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Description: mitochondrial NADH-ubiquinone oxidoreductase chain 6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cytochrome c oxidase subunit II"
/db_xref="PID:g1166532"
/transl_table=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xrefe"FlyBase:FBgn0013685"
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/db_xrefe"PID:g1166531"
                                                                                                                                                                                                                                                     /db_xref="FlyBase:FBgn0013685"
/product="tRNA-Cys (GCA)"
complement(1403..1468)
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"FlyBase:FBgn0013685"
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/db_xref="FlyBase:FBgn0013685"
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/product="tRNA-Lys (CUU)"
3840..3906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="FlyBase:FBgn0013685"
                                                                                                                                                                                                                                                                                                                                                                                                                          /product="tRNA-Tyr (GUA)"
1470..1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="tRNA-Leu (UAA)"
3083..>3767
                                                                                                                                                                                                                                  oxidoreductase chain 6"
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KEYWORDS

SOURCE

TITLE

TITLE

TITLE

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(bases 1 to 1837)
Valera,S., Hussy,N., Evans,R.J., Adami,N., North,R.A.,
Valera,S., Hussy,N., Evans,R.J., Adami,N., North,R.A.,
Valera,S., Hussy,N., Evans,R.J., Adami,N., North,R.A.,
A new class of ligand-gated ion channel defined by P2x receptor for extracellular ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MARRLQDELSAFFFEYDTPRMVLVRNKKVGVIFRLIQLVVLVYV
IGWVFVYEKGYQTSSDLISSVSVKLKGLAVTQLQGLGPQVWDVADYVFPAHGDSSFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MINITYTPOOTOGHCAENPEGGICODDSGCPPGKAERKAGGIRTGRCVPFNGTVKTCE
IFGWCPVEVDDKIPSPALLREAENFILFIKNSISFPRFKVNRRNLVEEVNGTYMKKCL
YHKIQHPLCPVFNLGYVVRESGODFRSLAEKGGVVGITIDMKCDLDMHVRHCKPIYQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGLYGEKNLSPGFNFRFRARHFVQNGTNRRHLFKVFGIHFDILVDGKAGKFDIIPTWTT
IGSGIGIFGVATVLCDLLLLHILPKRHYYKQKKFKYAEDMGPGEGEHDPVATSSTLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-APR-1996) H.J. Gilbert, Deptartment of Biological and Nutritional Sciences, Univ. of Newcastle upon Tyne, Newcastle, NE1
                                                                                     Norway rāt.
Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (21-70L-1994) G.N. Buell, Glaxo Inst of Mol Biology, 14
Chemin des Allx, 1228 Plan-les-Ouates, Geneva, SWITZERLAND
Location/Qualifiers
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2 (bases 1 to 1862)
Millward-Sadler,S.J., Hall,J., Black,G.W., Hazlewood,G.P. and
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Chytridiomycetes; Neocallimasticales; Neocallimasticaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.57e-01;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/cell_type="smooth muscle"
/clone_lib="pBKCMV plasmid cDNA library"
210..1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLN Piromyces sp. mRNA for endo-bl,4-mannanase. 91292878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endo-1,4 beta-mannanase; manC gene
                                                                                                                                                                                                                                                                                                               Nature 371 (6497), 516-519 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"PID:9558240"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="P2X"
/codon_start=1
                                                                ATP receptor; P2X gene
    R.norvegicus P2X mRNA.
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Best Local Similarity 72.3%;
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                                                                                                                                                                           Murinae; Rattus,
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Piromyces sp.
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                                                                                                                                                                                                                                                                                                                                                                               Buell, G.N.
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SMSVLAGKLQLVGTPAMLLASKPEBTPPEPVEFVYITDPTYTKKQVLANHILVLKVU
AFDLAAPTINQFLTQYELHQPRNCKTSELAMFLGELSLIDADPYLKYLPSVIAAAAF
HLALYTVTGQSWPESLVQKTGYTLETLKPCLLDLHQTYLRAPQHAQOSIREKYKNSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRVAPLKDLOINDEYVPYPPWKANKQPAFTIIYDBABEIGKRPTBSKKSBSEDVLAF
NSAVTLPGPRKPLAPLDYPWDGSFESPHTWEMSVVLEDEKPVSVNEVPDYHEDIHTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"EFQEDQENVNPEKAAPAQOPRTRAGLAVLRAGNSRGPAPQRPKT
                                                                                                                                                                                                                                                                                                       Submitted (08-SEP-1992) T. Hunt, ICRF Clare Hall Laboratories, SOUTH Mimms, Herts ENG 3LD, UK
2 (bases 1 to 1512)
Kobayashi, H., Stewart, E., Poon, R., Adamczewski, J. P., Gannon, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In the 'Structure' publication: The 5'end of clone A3 was made by PCR, and introduced a methionine in place of a valine, followed by a glycine to make an Nooi site. At the 3' end, an Xhoi site was engineered in to allow subcloning into pET21d, which also puts 6 histidines at the C-terminus that were used for purification. Location/Qualifiers
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                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
(bases I to 1512)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown, N.R., Noble, M.E., Endicott, J.A., Garman, E.F., Wakatsuki, S., Mitchell, E., Rasmussen, B., Hunt, T. and Johnson, L.N.
The crystal structure of cyclin, A
Structure 3 (11), 1235-1247 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="subunit structure=cyclin A /p34cdc2 or cyclin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1496 TATGAATGATGTTTGATTTAAATATAATACATATTAAAATGTATGGGGGGACCAAAAAA 1555
                                                                                                                                                                                                                                                                                                                                                                                                              Identification of the domains in cyclin A required for binding and activation of, p34cdc2 and p32cdk2 protein kinase subunits Mol. Biol. Cell 3 (11), 1279-1294 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1995
                       19-JUL-1996
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Pred. No. 1.57e-01;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 800
                       MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="PID:g10"
/db_xref="SWISS-PROT:P30274"
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                                                                                                         cyclin A; protein kinase activation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lymphocyte"
                                                                                                                            domestic cattle or domestic cow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="Cyclin A-3"
/db_xref="PID:e54213"
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    выса 1512 bp RNA
B.taurus mRNA for cyclin A.
X68321
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298 C 3:
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Best Local Similarity 72.3%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                      Bos taurus
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                                        DEFINITION
                                                                                                                                                 ORGANISM
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AUTHORS
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AUTHORS
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MEDLINE
COMMENT
                                                           ACCESSION
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FEATURES

CDS

RESULT LOCUS

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ORIGIN

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Gilbert, H.J.

Evidence that the Piromyces gene family encoding endo-1.4-mannanases arose through gene duplication

and fems microbiol. Lett. 241, 183-188 (1996)

Location/Qualifiers

Location/Qualifiers

1..1862

/organism="Piromyces sp."

1..110

/gene="manc"
/codon_start=1
/product="endo-1,4 beta-mannanase"
/db_xref="PiD: e1292879"
/db_xref="PiD: e129878"
/db_xref="PiD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 c
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Query Match
1.9%; Score 30; DB 64; Length 1862;
Best Local Similarity 69.7%; Pred. No. 4.73e-02;
Matches 62; Conservative 0; Mismatches 26; Indels 1; Gaps 355 g BASE COUNT ORIGIN

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Search completed: Thu Nov 6 11:06:27 1997 Job time: 1465 secs.

*****	(ТМ)	*****
在在古典中,我们的,我们的,我们也是我们的,我们的,我们的,我们的,我们的,我们的,我们也不会有什么的,我们的,我们的,我们的,我们的,我们的,我们的,我们的,		***************************************
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Thu Nov 6 11:06:47 1997; MasPar time 169.89 Seconds 962.007 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-842-827-3 (1-1566) from US08842827.seq 1566 Title:

Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

142080 seqs, 52183452 bases x Searched:

Dbase 0; Query 0

STD :

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq28 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28

Mean 9.622; Variance 6.597; scale 1.459 Statistics: Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query Match	Query Match Length DB	DB	1D	Description	Pred. No.
c 1	06	5.7	1047	7	010572	Human Natriuretic Pep	1.84e-34
7	7.1	4.5	1047	7	010572	Human Natriuretic Pep	9.34e-24
۳ ن	45	2.9	91	σ	051746	Oligonucleotide probe	7.85e-10
4	41	2.6	91	Φ	051746	Oligonucleotide probe	8.16e-08
S	40	5.6	204	Н	N81164	Base substituted E.co	2.56e-07
9	38	2.4	204	Н	N81164	Base substituted E.co	2.46e-06
7	36	2.3	114	12	070468	Generic DNA sequence	2.28e-05
ထ	36	2.3	114	12	970467	Generic DNA sequence	2.28e-05
<u>ი</u>	34	2.2	67	7	T14322	Primer used in the la	2.04e-04
10	3	7.7	114	12	970469	Generic DNA sequence	6.86e-05
#	34	2.5	114	12	070465	Generic DNA sequence	2.04e-04
12	34	2.2	114	12	970467	Generic DNA sequence	2.04e-04
c 13	35	2.2	114	17	070465	Generic DNA sequence	6.86e-05
c 14	34	2.2	114	12	070470	Generic DNA sequence	2.04e-04
c 15	34	2.5	114	12	070468	Generic DNA sequence	2.04e-04

2.04e-04 6.01e-04 1.75e-03 5.03e-03	1.75e-03 5.03e-03 4.00e-02	1.43e-02 4.00e-02	1.11e-01	1.11e-01 1.11e-01	8.04e-01	8.04e-01	3.01e-01	3.01e-01	8.04e-01 3.01e-01	8.04e-01	2.11e+00	2.11e+00	2.11e+00	2.11e+00	2.11e+00
Generic DNA sequence Ligand-induced gene, Generic DNA sequence Generic DNA sequence	Generic DNA sequence Clone GP3 encoding ma Generic DNA sequence	DNA	Generic DNA sequence	HCV envelope region n Human FceRI alpha qen	Mixed oligonucleotide DC43 TSAR library gen	TSAR library	Sequence encoding new	encoding	Sequence encoding new Interleukin-10 recept	Human stromalin-2 DNA	Sequence encoding new	Bovine vascular endot	Bovine VEGF-164 codin	specific	Genomic DNA from Plas
Q70469 Q42784 Q70466 Q70470	070466 041226 070472	070472	070471 070471 070471	035072	Q51787 T13613	T13611	N50034	N50023	N50033 Q69215	082834	N50026	010791	044259	N90224	N90733
12 12 12	12	175	177	ဖတ	21	217	m	'n	3	14	'n	7	7	Н	Н
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ALIGNMENTS

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010572;
09-ARR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; CNP; Kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
//Abbi-extracellular domain
//tote-"binds natriuretic peptides A,B and C]"
//tote-"binds natriuretic peptides A,B and C]"
//tote-"bomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- cytoplasmic domain
/note- "GC and protien kinase activity"
wodified site 24..26
/label- N-glycos_site
Modified -site 35..37
                                                                                                                                                                                                                                                                       Location/Qualifiers
010572 standard; DNA; 1047 BP.
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Domain 479..1047
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Modified -site 277..279
/label= N-glycos_site
Modified -site 349..351
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/label* N-glycos_site
Modified -site 195..197
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Wodified -site 244..246
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Modified -site 600.602
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Protein 12
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wo9100292-A.
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926 hannna-rmananndavssnrnrhrnhdnnrnrngvhtgnvcagvvgnkmnrycnngdtv 984
                                                                                  319 CAAGGCCGATGGAATGAGGTGCGGGACGACGGCCGAGGCCCTTGATTATCGAGCCCGGGC
                                                                                                                   ntasrmnsngnanknhvssttkdandnngcnnnnnrgdvnmkgkgkmr 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 71; DB 2; Louis Pred. No. 9.34e-24;
                                                                                                                                                                                                                                                                                                                                                                                                Domain 23..455
/label- extracellular domain
/note- "binds natriuretic peptides A,B and C]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- cytoplasmic domain
/note- "GC and protien kinase activity"
wodified -site 24..26
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                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Q10572 standard; DNA; 1047 BP
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label- transmembrane domain
Ocmain 479..1047
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8.9%;
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                                                                                                                                                                                                                                           09-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- N-glycos_site
Modified -site 35.37
/label- N-glycos_site
Modified -site 161.163
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!odified -site 349..351
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                                                                                                                                                                                                                                                                                                                                    Peptide 1..22
/label= signal sequence
Protein 12
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23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 CTGTCATGGTACGGATAGTTGATGCTGTTGTCTTTACAGAAAAGCCTCTCTGAAATGGA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                          208 ggnnnathnnrangrnvyncgnnnmnhnnnnnanrnntngdyvnnyndvngnsnragnt 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     976 AIGGATACGGCAACAAGACCAAATIGCAGIGIGGGGGGTAAGAGICIIGCCCAGICICCC 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 snmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrryhgvtgnvvmdknnd 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           858 AGTGGCCTGAATAGAAGGACAACCTGCCTTCCTTAACTCTTTCTGCATTCCCTCGACATA 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      678 TAGCAGCTGCACCAAATAAAAAGGTTCCAATGGCTTTGTAAATAGTGGCTATGTAGTTAT 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACTGATAAAGGAATTTGAGTGCAAAAGGTTACAGTAAACAG-ACAGGGTTTCTCCAAGA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 ntannnnsgnnnnttgmnaadvysngnnnnnnnrsgnnynngndnsnknnvnkvrngnr 745
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                                                                                                                                                                                                                                                                                                                                                                               148 kngnnvvtnhghnnwtaraannyndartddrnhyntnngvnnanngsnnsvnhnvyarnn 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1036 CCAGTCAACACCATCGCTCCAGTGGTGTTTATAATCAGAAACTCGAGAAAGGCCCACATAA 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 ratgrowndortrnnananrnanntvnvntyrnnnnnynnnnrnnnrarndngvnngn 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwykgannsdnnncandnddns 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              798 IGTAGTATTCAATGTAACCATCGCTGCAGTTGATTTTTGACCAATCTGGATCACAACAT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 hkgagsrntnsnrgssygsnmtahgkynnnantghnkgnvvankhvnkkrnnntrn-vnn 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nnkhmr-dvnnnhntrnngacndnnnncnvtnycnrgsnndnnnndsnnndwmnrysnnn 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 ATAATAGAGGAAACGGGCAAGCCAACCCCCACTAGGATGAGGACAGTGGGATGCGGCGGTA 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 TATATITGGCCCAATTTTAGAACAGCCATAGGCATGGAAGCCAGCAACACGCAGAGCACA 380
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                                                                                       Natilitetic protein receptor B - for diagnosis and treatment of kidney failure. heart failure, hyperaldosteronism, glaucoma etc. Claim 3: Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. Of the protein, opt. after being mutated to produce II4,952). The protein has a mol wt. of 115 kD (calculated Mrativity.) The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affility chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                    7; Gaps
                                                                                                                                                                                                                                                                                                                     DB 2; Length 1047;
                                                                                                                                                                                                                                                                                                                                                  74; Conservative 251; Mismatches 556; Indels
                                                                                                                                                                                                                                                                                       51 T;
                                                                                                                                                                                                                                                                                                                  5.7%; Score 90; DB 2; L
8.3%; Pred. No. 1.84e-34;
                                                                                                                                                                                                                                                                                       83 G;
                                                                                                                                                                                                                                                                                       15 C;
                                                                                                                                                                                                                                                                                   87 A;
                                (GETH ) GENENTECH INC.
22-JUN-1990; U03586.
23-JUN-1989; US-370673.
                                                                                                                                                                                                                                                                                   1047 BP;
                                             Chang M, Goeddel D, WPI; 91-036711/05. N-PSDB; 010324.
                                                                                                                                                                                                                                                                                                                                 Local Similarity
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Human Natriuretic Peptide Receptor B. NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase. National Control of the control of t Length 1047; 259 CGGGGCTGCCGACGCCCCGAGA-TACGGCCCCTCCCAGCCGGAGGAG 213 51 T;

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RESULT
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                                                                                                                                                              345 TITGACAAGACGCGGCTGCCGTACGTGGCCCTC-GATGTGCTCTGCGTGTT-GCTGGCTT 402
                                                                                                                                                                                        snnsvnhnvyarnnggnnnathnnrangrnvyncgnnnmnhnnnnnanrnnntngdyvnn 253
                                                                                                                                                                                                                                                                                                    nararndngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrry 373
                                                                                                                                                                                                                                                                                                                                                          hgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgann 433
                                             74 acsnynannsavdnknyhdndnnngngcvynaasvarnashwrnnnntagavasgnsakn 133
                                                                                                        287 GCCGTCCTCCACCTCATTCCATCGCCTTGCC-GG-GCAGCCCGGGCAGAGACCATG 344
                                                                                                                                     dhyrtnvrtgnsankngnnvvtnhghnnwtaraannyndartddrnhyntnngvnnanng 193
                                                                                                                                                                                                                                              254 yndvngnsnragntratgrnwndnrtrnnananrnanntvnvntyrnnnnnnynnnnrn 313
                            aggvrnngarnntnavvnnnhnnsyawawnrvgnavanavnangrannvdnrnvssnnng 73
Conservative 276; Mismatches 607; Indels 13; Gaps
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                                                                                                                                                                                                                                                                        462 TGTAAAGACAACAGCATCAACTATCCGTACCATGACAGTACCGCCGCATCCACTGTCCTC
                                                                                                                                                                                                                                                                                                                             522 ATCCTAGIGGGGTIGGCTIGCCCGITICCICIAITATICITGGAGAAACCCIGICIGI
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88;
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CT 3 Q51746 standard; cDNA; 91

RESULT ID 05

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1127 GGAGGACTCTCATACAACTCTGCATGAAACACCAACAACTGGGAATCACTATCCGAGCAA 1186
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but
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                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of 1 (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MX14+ consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 Bp; 5 %; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-WAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                      Oligonucleotide probe MKĪ4-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 9; Length 91;
Pred. No. 7.85e-10;
Tref. Trefles 6; Indels
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New oligo:nucleotide probes specific for Mycobacteria - u
detection and amplification of Mycobacteria nucleic acid
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Pred. No. 8.16e-08;
47; Mismatches 6; Indels
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                                                                                                                               01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.9%;
8.8%;
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Best Local Similarity 10.0%;
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N81164 standard; DNA; 204
  (first entry)
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                                                                                                                                                                                                                               Spears PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 BP;
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01-DEC-1993.
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31-MAY-1994
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Disclosure; p; English.
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P-PSDB; R65154.
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Thirducing random point mutations into nucleic acods -
Thirducing random point mutations and screening a primer, elongation,
maisincorporation, completion of molecules and screening.
The maisincorporation completion of molecules and screening.
The maisincorporation completions were introduced into the alpha fragment of Escoli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to to generate a popon of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.
The sequence covers all 176 difft base substitutions, most of which see also P80575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 GCTGGCGGTGGGAGCGCCGGCCCGGTCTCAGCCGGCCTCGTCGTCCTCCTCCTCCGGCT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 bnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccbnn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 GGGAGGGCCGTATCTCGGGGCCGTCGCAGCCCCGGCCCGGGCTCGATAATCAAGGCC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T; WPI: 88-279937/40. Introducting random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9ycgacbcyrraggnyccccggggywccgagcycgaayycdchvgccgymrttthhyrrmr 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NoV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
 galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                                                                                                                                                                                                                                                                                                108 Others;
                                                                                                                                                   (SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J, Kolvula A, Bamford J, Reinikainen
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 1; I
Pred. No. 2.56e-07
                                                                                                                                                                                                                                                                                                                                                                                                17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 TCGGCCGTCCTCCTCATTCCATCGCCC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 hychnyhbnnhrnwayvrhdarrddyhccychc 191
                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function=multiple cloning site primer_bind 187..204
                                                             /function-multiple cloning site primer_bind 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N81164 standard; DNA; 204 BP
                                                                                                                                                                                                                                                                                                                                                                                                21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.6%;
Best Local Similarity 17.0%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUSO) SUOMEN SOKERI OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1988;
30-MAR-1988; 105163.
03-APR-1987; US-034819.
                                                                                                              05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
                                       19..69
                                                                                                                                                                                                                                                                                                                                                                                                204 BP;
               007
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                                   misc_feature
                                                                                                EP-285123-A.
  beta
            Escherichia
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                                                                           primer bind
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recenting a recombinant vector library expressing fusion proteins
recenting a recombinant vector library expressing fusion proteins
recenting a recombinant vector library expressing fusion proteins
recomprising a binding domain and an effector domain

Disclosure, Pages 35, 3599; English.

Sold 68 is a generic DNA sequence used to generate random TSAR (Totally
COMPGES is a generic DNA sequence used to generate formula can also be
represented as follows: X(NNB) LIT(TCC) (NNB) 7 (TCC) (NNB) 10. X
and Y are flanking restriction sites (X is not the same as Y) that are
not specified further. Other generic sequences are shown in Q70466-68
other specific peptides generated by these generic sequences are shown in
RS5191-54. TSARs are concatenated by these generic sequences are shown in
RS5191-54. TSARs are concatenated by these generic or peptides
comprising at least two functional regions - a binding domain with
affinity for a ligand and a second effector peptide portion that is
chemically or biologically active. They may further comprise a linker
peptide between the 2 domains. The oligonuclectides are also designed so
that the expressed peptide contains 2 or 4 cysteine residues positioned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 yrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncnc 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 bgcaggycgacbcyrraggnycccggggywccgagcycgaayycdchygccgymrttthh 93
Random point mitations were introduced into the alpha fragment of E.coll beta-galactosidase. The wild type sequence was obtained as a single stranded template and an ollogoucleodtie was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which see also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 ccbnnhvchnvhbnnhrnwayvrhdarrddvhccvchcc 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GGCGCTCCCACCGCCAGCAATGGCGCCCCGGGGCCCTCCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; L
Pred. No. 2.46e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "this sequence represents 'Z'; Z can be sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 G;
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55..60
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 Match
Local Similarity 19.5%;
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 A;
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Tidentifying proteins or peptide(s) which bind a ligand - by
screening a recombinant vector library expressing fusion proteins
compitising a binding domain and an effector domain

Disclosure; Page 35: 255pp; English.

O70467 is a generic DNs sequence used to generate random TSAR (Totally
C70467 is a generic DNs sequence used to generate random TSAR (Totally
C70467 is a generic DNs sequence used to generate random TSAR (Totally
C70467 is a generic DNs sequence used to generate random TSAR (Totally
C70467 is a generic DNs STAND) IG(TGC) (NNB) IG(NNB) IG(NNB) IC (NNB) IG(NNB) IC (NNB) IC
C704 is a follows: X(NNB) IG(TGC) (NNB) IC (NNB) IC (NNB) IC
C704 is a further. Other generic sequences are shown in O70466-68.
C705 is a legal of the generated by these generic sequences are shown in O70466-68.
C706 is a legal of the sequence of concatenated heterofunctional proteins or peptides,
C706 is a legal of a second effector peptide portion that is
C707 in or inpantally active They may further comprise a linker
C708 in or ilanking, the unpredicted or variant residues residues
C709 in or ilanking, the unpredicted or variant can be used in vivo to compana companially or biologically active may expense the conformational rigidity to the peptides. These residues or companial c
                     confer some degree of conformational rigidity to the peptides. The TSARS or composins, comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, e.g. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARS are easily characterised and have designed activity sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deliver a chemically or biologically active moiety, eg. metal ion, radioloscope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for
                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flanking, the unpredicted or variant residues. These residues
                                                                                                                                                                                                                                                                                                                                                                                                                                               3 banbanbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbananan 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generic DNA sequence to generate a random TSAR petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 CCGGTCTCAGCCCGCCCTCGCTCTCCTCCTCCGGCTGGGAGGGGCCCGT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 bunbunbunbunbunbtgcnnbunbnnbunbunbunbunbunbunbunb
                                                                                                                                                                                                                                                                                                                                      DB 12; Length 114;
                                                                                                                                                                                                                                                                                                                                   Score 35; DB 12; Length 114;
Pred. No. 2.28e-05;
34; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents 'Z'; Z can be 5, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
FOWIKES DM, KAY BK; WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                   2.3%;
Similarity 3.6%;
4; Conservative
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01-FEB-1993; US-0134
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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/note= "this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                   Query Match
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Disclosure: Page 19; 71pp; English.

Disclosure: Page 19; 71pp; English.

C Determining the nucleotide sequence (I) of a target polynucleotide (T) comprises: (a) generating from T a plurality of fragments that cover T; (b) attaching an oligonucleotide tag from a repertoire of tags, to each fragment such that all the same fragments have the same tag, and all different fragments have different tags; (c) sorting the fragments by specifically hybridising the tags with their respective tag complements; (d) determining (I) of a portion of each of the fragments: and (e) determining (I) of T by collating the sequences of the fragments. The tagging system can be used with single hase sequencing methods to sequence polynucleotides up to several kilobases in length. The tagging system permits many thousands of fragments of a target polynucleotide to be sorted onto the sequence represents and sequenced simultaneously. This sequence represents a primer which could be used to reverse transcribe mRNA. If the amplified product is then needed to be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP: 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Labelling and sorting mols. using ollgo:nucleotide tags – useful in large-scale parallel operations, e.g. DNA sequencing and mRNA \,
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attached to a solid phase support a sequence like the one given in T14323 may be used. The mRNA would then be removed and the second strand of cDNA produced using a primer with a similar form to that described in T14324. After restriction enzyme digestion, the conjugate would have the formula described in T14325. Sequence 67 BP; 3 A; 13 C; 4 G; 20 T;
                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-1997 (first entry)
Primer used in the labelling and sorting of nucleotide molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                        84 GCTCTGTAGCCTCAGGACCTCCTCAGCCGGCACGGCCTGCCCGGTTGCTAC 33
                                                                                               Score 36; DB 12; Length 114; Pred. No. 2.28e-05; 32; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 24; Length 67;
Pred. No. 2.04e-04;
23; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Labelling; sorting; sequencing; tag; tagging; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LYNX-) LYNX THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                           T14322 standard; DNA; 67 BP
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/mod_base= Linked to biotin
                                                                                               2.3%;
Similarity 5.4%;
6; Conservative
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Similarity 38.9%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1995; U12678.
13-OCT-1994; US-322348.
19-DEC-1994; US-359295.
                                                                                               Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                  T14322;
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RESULT

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sequence represents 'Z'; Z can be 6, 9 or 12 nucleotides (see

US-013416

Location/Qualifiers 55..60

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PI FOWINGS DM, Kay bk;

WRI; 94-279739/34.

BR PPSDB; R65150 and R65151.

PT Identifying proteins or peptide(s) which bind a ligand - by

T dentifying proteins or peptide(s) which bind a ligand - by

T comprising a binding domain and an effector domain

PT Sorcening a recombinant vector library expressing fusion proteins

PT SISCISORNE; SPAGE 51-575p; Bng11sh.

COUNTIST Affinity Reagents) peptides. This generic formula can also be

CC Synthetic Affinity Reagents) peptides. This generic formula can also be

CC Synthetic Affinity Reagents) peptides. This generic formula can also be

CC Comprising restriction sites (X is not the same as Y) that are

not specified further. Other generic sequences are shown in Q70466-68.

CC Cher specific peptides generated by these generic sequences are shown in

R65151-54. TSARs are concatenated by these generic sequences are shown in

R65151-54. TSARs are concatenated by these generic sequences are shown in

R65151-54. TSARs are concatenated by these generic sequences are shown in

R65151-54. TSARs are concatenated by these generic sequences are shown in

R65151-54. TSARs are concatenated by these generic sequences are shown in

R65151-54. TSARs are concatenated by these generic sequences are also designed

CC memically or biologically active. They may further comprise a linker

CC peptide between the 2 domains. The oligonucleotides are also designed

CC that the expressed peptide contains 2 or 4 cysteine residues positioned

CC or compsns. comprising a TSAR binding domain can be used in vivo to

deliver a chemically or biologically active molety, eg. metal ion,

CC deliver a chemically or biologically active molety, eg. metal ion,

CC complex methods of phyridoma formation or nive cell. They can also replace the function of marcomolecules, eg.

CC complex methods of phyridoma formation or nive specific target or on the

CC for complex methods of phyridoma formation or nive seconics methods of phyridoma formation or nive residues

CC activity allowing direct and rapid detection i
                                                                                                                                                                                                                                                                        30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UINC-) UNIV NORTH CAROLINA.
FOWlkes DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                               sequence of 6,
                                                                                                                                                                                                   18-AUG-1994.
01-FEB-1994; t
01-FEB-1993; t
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/note= "this
                                                  misc_feature
                                                                                                                                                                            WO9418318-A
       Synthetic.
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Which 194-2/1939/34.

Transity 194-2/1939/34.

Transity a compinant vector library expressing fusion proteins compitising a binding domain and an effector domain proteins.

Disclosure: Page 35: 255pp: English.

Disclosure: Page 35: 255pp: English.

This generic Pormain and be represented as follows. 7(TGC)(NNB)10-

This generic formula can be represented as follows. 7(TGC)(NNB)10-

Transity of the same as Y) that are not specified further. This sequence generic specifies that are cloveribed in structure. Other generated by these generic sequences are shown in 70/465-68. Other specific peptides generated by these generic sequences are shown in 70/465-68. Other specific peptides generated by these generic sequences are shown in 70/465-68. Other specific peptides concatenated heterofunctional proteins or peptides. Comprising at least concatenated heterofunctional proteins or peptides. Comprising at second effector peptide portion that is chemically or biologically active rhey may further comprise a linker peptide between the 2 domains.

The oligonic lectides are also designed so that the expressed peptide conformational rigidity to the peptides. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsis. Comprising a TSAR binding domain can be used in vivo to deliver a chemically or or enzyme, to the specific target or on the cell. They can also replace the function of macromolecties, eg. monoclonal or polyclonal antibodies conformation or in vivo antibody process.

Commation or in vivo antibody process.

Conformation or in vivo antibody process.

Conformation or in vivo antibody process.

Conformation or in vivo antibody accounting a are easily characterised and have designed activity allowing direct and rapid
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                                                                          Generic DNA sequence to generate a random TSAR peptide library. TSAR: totelly synthetic affinity reagent: synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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  standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOwlkes DM, Kay BK:
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
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/note- "this
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106 GCCTCGGCACTAACCGAGTGTTCGCGGGGCTGTGAGGGGAGGGCCCCGGGCGCCATTGC 165
                                                                         Generic DNA sequence to generate a random TSAR petide library.
TSAR, totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heresfertofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                       Gaps
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                                                                                                                                                  63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnb 114
                                                                                                                                                                                    166 TGGCGGTGGGAGCGCCGCCCGGTCTCAGCCCGCCCTCGGCTGCTCCTCCT 217
 Score 34; DB 12; Length 114;
Pred. No. 2.04e-04;
33; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                          Q70467 standard; DNA; 114 BP.
2.2%;
Similarity 3.6%;
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2 gcnnbanbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbannan 61

쉱 à 셤 ö 05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.

Q70465 standard; DNA; 114 BP. Q70465;

RESULT ID 07 AC 07 DT 05 DE GE KW 15 KW ef

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misc_feature
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                                                                                                                                                                                                                                          referently a recombinant vector library expressing fusion proteins screening a recombinant vector library expressing fusion proteins screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins bisclosure, Page 35: 255pp; English.

7070467 is a generic DNA sequence used to generate random TSAR (Totally 7070467 is a generic DNA sequence used to generate communication of proteins of proteins and the flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in 7070466-68.

70 ther specific peptides generated by these generic sequences are shown in R55151-54. TSARs are concatenated beforefunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonuclectides are also designed on that the expressed peptide contains 2 or 4 cystelne residues positioned in compense compense of conformational rigidity to the peptides. These residues or compense compense of conformational rigidity to the peptides. The TSARs in TSARs in the compense of compense of conformational rigidity to the beytides. The TSARs of the compense of compense of conformational rigidity to the beytides.
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TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        direct and rapid defection in a screening process Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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                                           01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UINC-) UNIV NORTH CAROLINA.
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WPI; 94-279739/34.
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PPT Gentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PPT Gentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PPT Screening a recombinant vector library expressing fusion proteins

PPT Screening a plading domain and an effector domain

PPT Screening a sequence used to generate random TSAR (Totally

COTOMAS STATEMENT AFFINITY REAGENTS) PEPTIGESTHIS GENERAL STATEMENT AFFINITY REAGENTS) PEPTIGESTHIS GENERAL SAME AS A SCREENING SCREENING SCREENING STATEMENT AFFINITY REAGENTS (NNB) (TGC) (NNB) 112 (NNB) 14 (TGC) (NNB) 13. X

AND X are flanking restriction sites (X is not the same as Y) that are not x peptide further. Other generic sequences are shown in COTOMAS are concatenated beterofunctional proteins or peptides.

CC THER SPECIFIC PEPTIGES GENERAL SEASON IN 1070466-68.

CC COMPISSING A LEAST WO functional regions - a binding domain with a finity for a ligand and second effector peptide portion that is comparised between the 2 domains. The oligonucleotides are also designed to that the expressed peptide contains 2 or 4 cysteine residues positioned in or flanking, the unpredicted or variant residues reasones residues confer some degree of conformational rigidity to the peptides. The TSARS or compension a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, calliver a chemically or biologically active moiety, eg. metal ion, calliver be perided to replace the function of macromolecules, eg.
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070470 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker;
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Pred. No. 6.86e-05;
33; Mismatches 72; Indels
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/note= "encoded by Z (see comments)"
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31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM. KAY BK:
WPI; 94-279739/34.
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Best Local Similarity 3.7%;
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WPI; 94-279739/34.
P-PSDB; R65150 and R65151.
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01-FEB-1994;
01-FEB-1993; U
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represented as Lollows: Alternal Processing Science (CAC)2 (NNB)Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. The peptides generated by this and other generate sequences (OT04173) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated by this and concorporated into variant sequences. TSARs are concatenated the fractional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chanically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or compsus. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, and compsus. comprising a TSAR binding domain can be used in vivo to call they can also replace the function of macromolecules, eg. monoclonal or polytohal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
   as follows: X(NNB)4(CAC)(NNB)4(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8
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ö 0; Gaps Length 114; Score 34; DB 12; Length 114; Pred. No. 2.04e-04; 29; Mismatches 72; Indels Ouery Match
2.2%;
Best Local Similarity 9.8%;
Matches 11; Conservative Query Match m 윱

150 GCCCTCCCTCACAGCCCCCGCGAACACTCGGTTAGTGCCGAGGCGCTCGTGTGCCAGCC 91

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90 GCGGCAGCTCTGTAGCCTCAGGACCTCCTCAGCCGGCACGGCCTGCCCCGGT 39

Generic DNA sequence to generate a random TSAR petide library.
TSAR: tocally synthetic affinity resegnt; synthetic; binding domain;
effector domain; concatemented heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss. Location/Qualifiers 55..60 JT 15 Q70468 standard; DNA; 114 BP. 05-APR-1995 (first entry) Synthetic.

/note- "this sequence represents '2'; Z can be a sequence of 6, 9 or 12 nucleotides (see 01-FEB-1994; U00977. 01-FEB-1993; US-013416. comments)"

misc_feature

/*tag=

(UYNC-) UNIV NORTH CAROLINA. Fowlkes DM, Ray BK; WPI; 94-279739/34. 31-JAN-1994; US-189331 P-PSDB; R65154

recenting a recombinant vector library expressing fusion proteins screening a recombinant vector library expressing fusion proteins screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins of screening a binding domain and an effector domain brackers. Page 33, 255pp; English.

7070468 is a generic DAN sequence used to generate random TSAR (Totally Cynthetic Affanity Reagents) peptides. This generate formula can also be represented as follows: X(NNB)117GC)(NNB)7CTC)(NNB)7CTC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q0466-68.

70 ther specific peptides generated by these generic sequences are shown in R5515-54. TSARs are concented by these generic sequences are shown in R5515-54. TSARs are concented a Comprising at least two functional regions - a binding domain with a fillity for a ligand and a second effector peptide portion that is chemically no biologically active. They may further comprises a linker chemically no biologically active. They may further comprise a linker between the 2 domains. The oligonoclectides are also designed to that the expressed peptide contains 2 or 4 cysteine residues positioned

in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity sequence 114 BP; 0 A; 2 C; 2 G; 2 T; 8888888888888

Gaps ; DB 12; Length 114; Score 34; DB 12; Length 114; Pred. No. 2.04e-04; 32; Mismatches 75; Indels 2.2%; Similarity 4.5%; 5; Conservative Query Match Best Local Similarity Matches

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177 CTCCCACCGCCAGCAATGGCGCCCGGGGCCCTCCCCTCACAGCCCCCGGGAACACTCGGT 118 ď

63 baabaabaabaabaabtgcaabaabaabaabaabaabaabaabaabaab 114

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Search completed: Thu Nov 6 11:10:04 1997 Job time: 197 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

. n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

Run on:

Thu Nov 6 11:10:33 1997; MasPar time 829.51 Seconds 969.077 Million cell updates/sec not generated. Tabular output

.........CCAAAAAAAAAAAAA 1566 >US-08-842-827-3 (1-1566) from US08842827.seq 1566 1 CCTGTGGGAGAGAGCGCCGG. Description: Perfect Score: N.A. Sequence: Comp: Title:

TABLE default Gap 6 Scoring table:

Gap

Dbase 0; Query 0 .. STD Nmatch

707517 seqs, 256659390 bases x 2 Minimum Match 0% Listing first 45 summaries Post-processing:

Searched:

Database

| 1.EST1 2.EST2 3.EST3 4.EST4 5.EST5 6.EST6 7.EST7 8.EST8 9.EST9 10.EST10 11.EST11 12.EST12 13.EST13 14.EST14 15.EST14 15.EST13 14.EST14 15.EST14 15.EST14 15.EST14 15.EST14 15.EST14 15.EST15 16.EST20 21.EST20 21.EST16 17.EST17 19.EST19 20.EST20 21.EST21 22.EST32 24.EST30 34.EST30 34.EST30 35.EST33 34.EST31 3

2 113:EST113 114:EST114 7 118:EST118 119:EST119 7 128:EST128 124:EST129 7 128:EST128 129:EST129 7 138:EST138 139:EST134 7 138:EST138 139:EST134 2 143:EST143 144:EST144 153:EST153 154:EST154 158:EST158 159:EST159 163:EST163 164:EST164 148:EST148 149:EST149 168:EST168 169:EST169 EST-STS-TWO 100:EST100 101:EST101 102:EST102 10 105:EST105 106:EST106 107:EST107 101 110:EST110 111:EST111 112:EST107 101 110:EST115 116:EST111 112:EST117 111 120:EST120 121:EST121 122:EST127 121 125:EST125 126:EST127 121 130:EST130 131:EST131 132:EST137 131 135:EST135 136:EST136 137:EST137 131 167:EST167 172:EST172 140. EST140 141: EST141 141 145. EST145 141 145. EST145 146 147 155. EST151 151 155. EST155 156. EST156 151 160. EST160 161. EST161 161 170: EST170 171: EST171 170

Database

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179:EST179
184:EST184
189:EST189
194:EST194
175:EST175 176:EST176 177:EST177 178:EST178 180:EST180 181:EST181 182:EST182 183:EST183 185:EST182 188:EST183 185:EST180 191:EST190 192:EST190 192:EST191 192:EST192 193:EST193 195:EST193 195:EST193 196:EST195 196:EST195
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Variance 2.886; scale 4.094 Mean 11.818; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

12-DEC-1995 yx03b06.s1 Homo sapiens cDNA clone 260627 3'. 91118455 RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE

human clone=260627 primer=m13 -40 forward library=Soares melanocyte

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AA043085 545 bp mRNA EST 04-SEP-1996
2k48802.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone
486027 5'.
AA043085
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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Fig. 1310 286 1
1189 TGATTGCTCGGATAGTGATTCCCAGTTGTTGGTGTTTCATGCAGAGTTGTATGAGAGTCC 1130
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                                                420 tectectttecttettaaaagaagttetteettgaagaaateegatacatatacagea 479
                                                                                                                                                       480 actaatattgcaaccagagctccctgaatgagtccagtcaacacatcgctcccagtgggg 539
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Huldman,M., Kucaba,T., Soares,M., Tan,F., Parsons,J., Riftin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Pred. No. 0.00e+00;
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                 Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata,
Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes,
Sarcopterygii, Choanata, Tetrapoda, Anniota, Mammalia, Theria,
Sarcopterygii, Choanata, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 587)
Hiller, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lenon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
High quality sequence stops: 351
Source: IMAGE Consortium, ELNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infodimage.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1368 ACTGAGTTAAAGGTAACTATGTACACACAAAGTGTGCATCCAAGAGGCATATCAGCAGCA 1309
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2NbHM vector-pT7T3D (Pharmacia) with a modified polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pi7r3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

/clone=472053
/clone=20ares pregnant uterus NbHPU"
/note-"Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I
                                                                                                                                                                                                                                                                                                                                                                                                                       1132 TCCTCCTCTTTTCTTTCTTTTAAAAGAAGTTCTTTCTTTGAAGAAATCCGATACATATACA 1073
                              1431 TGGGGCACTGTTTTGGTGGAAGGCTTGGAGTTTTTTAATGAGTTTAGAGCTATTAGATA 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W67667 546 bp mRNA EST 15-OCT-1996
2d38ml1.sl Soares fetal heart NDHH19W Homo sapiens CDNA clone
342998 3'.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                 Length 552;
                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                 Score 507; DB 159;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                           complement(<1..>552)
105 c 110 g
                                                                                                                                                                                                         /sex="female"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                 32.4%;
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.5%;
Matches 533; Conservative
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Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 452.
Location/Qualifiers
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Homo sapiens cDNA clone
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           942 CCCACACTGCAATTTGGTCTTGTTGCCGTATCCATTTATGTGGGCCTTTCTCGAGTTTCT 1001
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Bukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 552)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Ruchan,M., Ruchanda,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                  181 aaagaggaggactctcatacaactctgcatgaaacaccaacaactgggaatcactatccg
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Washu Marck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
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pregnant uterus NDHPU
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472063 3'.
AA036943
AR036949
91510000
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RESULT

DEFINITION

ACCESSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

source

FEATURES

480

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2x48b02.sl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 48602.3 3/- AA040858 91517154
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40Ml3 fwd, from Amersham
High quality sequence stop: 354.
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                                                                                                                        1055 CAGAGCTCCCTG-AATGAGTCCAGTCAACATCGCTCCAGTGGTGTTTATAAATCAGAAA 997
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rithin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Hohldmann,P. and
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                                                                                                                                                          481 ccccgagaaaggccacataaatggatacggcaacaagaccaaattgcagtgtgggg 536
                                                                                                                                                                               Contact: Wilson RK
WashUn/Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.00e+00;
0; Mismatches 3;
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/lab_host="DH10B"
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Local Similarity 99.4%;
les 462; Conservative
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ORIGIN
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JOURNAL
COMMENT
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Lengih: 634 Std Error: 0.00
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             1 (bases 1 to 546)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Hallman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Waltful, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                  Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/lab_host="DH10B (ampicillin resistant)"
complement(<1..>546)
105 c 121 g 159 t 2 other
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/clone_llb="Soares fetal heart NDHH19W"
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                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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High quality sequence stop: 321.
Location/Qualifiers
                                                                                                                    The WashU-Merck EST Project
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                                                                                                                                       Unpublished (1995)
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2843909.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
W04968 g
g2277708
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Washington University School of Medicine
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 315 286 1800
Fax: 315 286 1800
Fax: 315 286 1800
Fax: 315 286 1800
Fax: 316 386 1800
                                                                                                                                                                                                       1488 TATTACATACATGTTTATACATAAGCATTACATTTTTTTAATAAAATGTATACAGGTGG 1429
                                                                                                                                                                                                                                                                                                              300
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulbman,M., Rucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Ritkin,L., Rohlfing,T., Soares,M., Tan,F., Tan,F., Tan,F., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                    tattacatacatgtttatacataagcattacattttttaataaaatgtatacaggtgg
                                                                                                                                                                                                                                                                                                           241 gaagtetttaaaggettgtacaccaggaagaaagatgcatectettgeettgtggeaate
                                                                                                                                                                                                                                                                                                                                                                                                       301 attttcctttagaaaaaaggccagcttcacctgggcaccctgctgcctttcaaggctggt
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double-stranded cDNA was size selected, lighted to ECC RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Ecc RI sizes of a modified pTT73 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 bp mRNA EST 10-JAN-1996
Homo sapiens CDNA clone 265309 5' similar to WP:T28D9.3
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Bukaryotae: Metazoa: Eumetazoa: Bilateria; Coelomata: Osteichthyes;
Deuterostomia; Chordata; Vertebrata; Gnathostomata: Osteichthyes;
Sarcopterygi; Chosnata; Terrapoda: Anniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

Hillier.L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 ccaggatgaagggagactgggcaagactcttacgccccacactgcaatttggtcctgttg 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549 ICCTCTATTATTCTTGGAGAAACCCTGTCTGTTACTGTAACCTTTTGCACTCAAATTCC 608
                                                                                                                                                                                                                                                                                                                                                                                                                           tttatcaggaataactacatagccactatttacaaagccattggaacctttttatttggt 156
                                                                                                                                                                                                                                                                                                                      96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcagctgctagtcagtccctgactgacatttgccaagtattcaataggcagactgcggcc
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                                                                                                                                                                                                                                                                   5
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post.conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                Length 472;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                             Score 413; DB 114;
Pred. No. 0.00e+00;
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COMMENT

FEATURES

ORIGIN

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Contact: Wilson RK
Washinderck EST Project
Washinderck EST Project
Washinderch EST Project
Washinderch University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 634 Std Error: 0.00
Seq primer: mob. REGA+ET
High quality sequence stop: 328.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .075 TATATGTATCGGATITCTTCAAAGAAGAACTTCTTTAAAGAAAGAAAGAGAGGGGGGCT 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 tiggicitgitgccgiatccatttatgigggcctttctcgagtttctgattataaacacc 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 tttatcttcaagccaggatgaagggagactgggcaagactcttacgcccacactgcaat 61
                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Overebrates, Butheria; Primates; Catarrhini; Hominidae; Homo. [ kases 1 to 446) Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rittin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 actggagcgatgtgttgactggactcattcagggagctctggttgcatattagttgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="342908"
/clone_lib="Soares fetal heart NDHH19W'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 406; DB 171;
Pred. No. 0.00e+00;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.9%;
Matches 431; Conservative
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     Homo sapiens
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AUTHORS
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                                                                                                                                                                                                              High quality sequence stops: 385
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1082 ATCGGATTTCTTCAAAGAAGTTC-TTTTAAAGAAAGAAAG-AGGAGGACTCTC-A 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          962 TGTTGCCGTATCCATTTATGTGGGCCTTTCTCGAGTTTCTGATTATAAACACCCACTGGAG 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttacattgaatactacatatgtcgagggaatgcagaaanngttaaggaaggcaggttgtc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 atcggatttcttcaaagaaagaacttccttttaaagaaaagaaaaggaggactctcca 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels 10; Gaps
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fex: 314 286 1810
Email: est@wastson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 414; DB 92;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                  138
                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/clone="265309"
<1..>490
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                                 The WashU-Merck EST Project Unpublished (1995)
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Best Local Similarity 97.1%;
Matches 476; Conservative
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Length 446; 1; Indels 181

1135 CTCATACAACTCTGCATGAAACACCAACAACTGGGAATCACTATCCGAGCAATCACCAGC 1194

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302 cttgaaaggcagcagggtgcc-aggtgaagctggcctgttttctaaaggaaaatgattgc 360

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Washington University School of Medicine
4444 Forest Park Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
This clone is awailable royalty-free through LLNL; contact the
IMAGE Consortium (infolmaqe.llnl.gov) for further information.
Insert Length: 728 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 435.
Location/Qualifiers
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                                                                                                                                                                  W45106 456 bp mRNA EST 10-OCT-1996
2C21a10.r1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA
Clone 322938 5'.
1255 CACAAGGCAA-GA-GGATGCATCTTTCTTCCTGGTGTACAAGCCTTTAAAGACTTCTG-C 1311
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Bukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 456)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hulfman,M., Nucaba,T., Le,M., Lennon,C., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                           361 cacaaggcaaaggaaggatgcatctttcttcctggtgtacaagcctttaaagacttctggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares senescent fibroblasts NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 0.00e+00;
0; Mismatches 1;
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W01275 474 bp mRNA EST 18-APR-1996
za40f11.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
295053 5' similar to contains element MER12 repetitive element ;
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This clone is available royalty-free through LLNL; contact the
IMAGE Conscritum (info@image.llnl.gov) for further information.
Seq primer: ETPT.int
High quality sequence stop: 429.
Location/Qualifiers
                                                          375 tgccacaaggcaagaggatgcatctttcttcctgggttgtacaagccttttaaagacttc 434
                                                                                                                                        315 ccttgaaaaggcagcagggtgcccaggtgaagctggccttgttttctaaaggaaaatgat 374
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Rultman,M. Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rhithir., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                      255 teteatacaactetgeatgaaacaecaacaactgggaateactateegageaateaceag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                       1..474
/organism="Homo sapiens"
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Email: est@watson.wustl.edu
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Best Local Similarity 98.3%;
Matches 415; Conservative
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                                                                                                                                         61 atgtgggcctttctcgagtttctgattataaacaccactggagcgatgtgttgactggac 120
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Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 422)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                    Score 406; DB 113; Length 4/4;
Pred. No. 0.008+00;
.....marches 6; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
Hash Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
<li..>474
                                                6 others
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1 Similarity 96.7%;
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human clone-211821 primer-M13RP1 library-Soares fetal liver spleen
human clone-211830 (Pharmacia) with a modified polylinker
host-DH10B (ampicillin resistant) Rsitel-Pac I Rsite2-Eco RI Liver
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 728 Std Error: 0.00 Seq primer: mob.REGAET High quality sequence stop: 160.
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/lab_host="balds (ampicillin resistant)"
complement(41.342)
73 c 90 g 133 t 2 others
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yr83f11.rl Homo sapiens cDNA clone 211821 5'
H68363
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Pred. No. 0.00e+00;
0; Mismatches 4;
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double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr713 vector. Library went through one round of normalization. Library
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                                                                           2141902.rl Soares pregnant uterus NbHPU Homo sapiens CDNA clone 504530 5'.
AA152123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mashington niversity School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Fax: 314 286 1810
Fax: 318 317
Fax: 318 318
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Fax: 318 31
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 471)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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/clone="504530"
/clone_lib="Soares pregnant uterus NbHPU"
/sex="female"
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/lab_host="DH10B"
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WashU-Merck EST Project
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Matches 447; Conservative
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Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choemata; Tetrapoda; Anniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lenon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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High quality sequence stops: 379
Source: IMAGE Consortium, LINI.
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1810
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Matches 436; Conservative
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Indels 11; Gaps 10;

Length 471;

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LOCUS W24605 415 bp mRNA EST 20-AUG-1996
DEFINITION 2b63f08.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 308295
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 773 Std Error: 0.00
                                                                            1193 GCCTTGAAAGGCAGCAGGTGCCCAGGTGAAGCTGGCCTGTTTTCTAAAGGAAAATGATT 1252
                                  953 ATTIGGICTIGITGCCGIAICCATTIAIGIGGGCCTTTCTCGAGTTICTGATTAIAAACA 1012
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Busaryotes mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Entheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 415)

1 (bases 1 to 415)

1 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Rucabb, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Washb-Merck EST Project
Unpublished (1995)
      1 atttggtctngttgccgtatccatttatgtgggcctttctcgagtttctgattataaaca
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
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1 (bases i to 479)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Tenno,G., Marra,M., Parsons,J., Rifkin,L., Rohliing,T., Soares,M., Tan,F.,
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Tel: 314 286 1800
Fax: 314 286 1810
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WashU-Merck EST Project
Washington University School of Medicine
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/clone="240696"
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High quality sequence stops: 364
Source: IMAGE Consortium, LLNL
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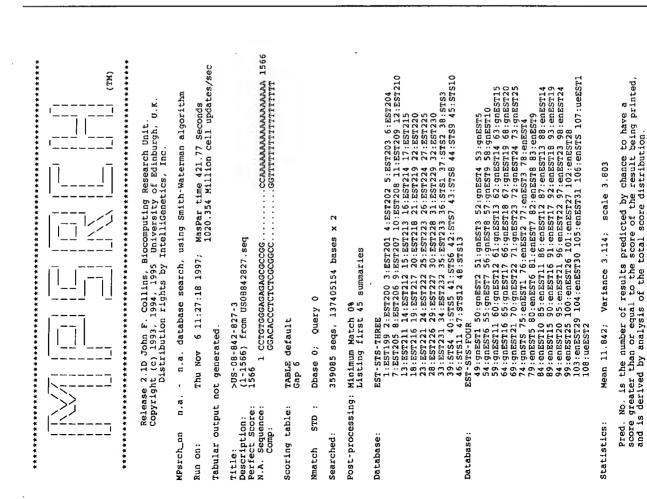
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(Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH19w."
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SUMMARIES

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Email: est@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28Mil rev2 from Amersham.
Location/Qualifiers
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Hillier, Clark, N., Dubbuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                                                                                                                                                                                                                                                                                                               Contact: Wilson RK Washin-Merck Est Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
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/lab_host="SOLR cells (kanamycin resistant)"
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Fex: 314 286 1810
Email: estwatson, wustl.edu
Email: estwatson, wustl.edu
Infostewatson, wustl.edu
IMAGE Consortium (infostmage.llnl.gov) for further information.
Insert Length: 600 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
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      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/lab_host="DH10B (ampicillin resistant)"
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/clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
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/organism="Homo sapiens"
//organism="Open Vector: pBluescript SK-; Site_1:
//note="Organ: colon; Vector: pBluescript SK-; Site_1:
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Washington University School of Medicine
Mathington University School of Medicine
444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                  1291 CAAGCCTTTAAAGACTTCTGCTGCTGATA-TGCCTCTTGGATGCACACTTTGTGTGTGTACA 1349
1174 ACTATC--C-GAGGAATCACCAGCCTTGAAAGGCAGGAGGGTGCCCAGGTAAAGCTGGCC 1230
                                                                                                                                                             1231 IGITITCIAAAGGAAAATGATIGCCACAAGGCAAGAGGATGCAICTITCIICCIGGIGIA 1290
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2020008.s1 Stratagene colon (#937204) Homo sapiens CDNA clone
AA132534
91694041
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Halliler, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Tan, P., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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                                                                                                241 tgttttctaaaggaaaatgattgccacaagn-aagaggatgcatctttcttcctggtgta
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complement(<1..>376)
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0; Mismatches 2; Indels
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/clone_lib="Stratagene colon (#937204)"
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Best Local Similarity 98.9%;
Matches 373; Conservative
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                                                                                                                                                                                                                                                                                                                    09-MAY-1996 (Rel. 47, Created)
07-MAR-1997 (Rel. 51, Last updated, Version 2)
2D63f08.rl Soares fetal lung NDHL19W Homo sapiens cDNA clone 308295
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.00e+00;
0; Mismatches 3; Indels
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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BP; 124 A; 87 C; 86 G; 116 T; 2 other;
                 /organism-"Homo sapiens"
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AA062861 377 bp mRNA EST 02-FEB-1997
zf70e10.sl Soares pineal gland N3HPG Homo sapiens cDNA clone 382314
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/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
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                                                                                                                                                                                                                                                                             This close is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length; 613 Std Error: 0.00 Seq primer: -40M13 Fwd. from Amersham High quality sequence stop: 333.
                                                                                                                                                                                                         1312 AGCAGAAGTCTTTAAAGGCTTGTACACCAGGAAGAAAGATGCATCCTCTTGTGTGGC 1253
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Budaryotae mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Butheria; Primates; Catarrhini; Hominidae; Homo.

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Hillar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Ten, F., Trevaskis, E., Washu-Merck Est Project
Unpublished (1995)
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WashDrwarck Exp Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. L
711: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                   Score 352; DB 28;
Pred. No. 0.00e+00;
0; Mismatches 1;
                    u
                  121
complement(<1..>378)
68 c 75 g
                                                                 Query Match
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Best Local Similarity 99.2%;
Matches 365; Conservative
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 600 Std Error: 0.00
Seg primer: -40M13 fwd. from Amersham
High quality sequence stop: 341.
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2e78b09.s1 Soares fetal heart NbHH19W Homo sapiens CDNA clone
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Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Mashu-Merckerston, K., Williamson, A., Wohldmann, P. and Wilson, R., Washu-Marck EST Project
Unpublished (1995)
                                                                                 Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
WashIngton University School of Medicine
Tel: 314 286 1800
Fex: 314 286 1810
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/clone_lib="Soares fetal heart NDHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                              1378 ATAGCTCTAAACTCATT 1394
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1 (bases 1 to 385)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Masra,M., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through Lini; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length; 807 Std Error: 0.00 Seq primer: -28M1 rev2 from Amersham High quality sequence stop: 213. Location/Qualifiers Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1186 ATCACCAGCCTTGAAAGGCAGCAGGGTGCCCAGGTGAAGCTGGCCTGTTTTCTAAAGGAA 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1306 TTCTGCTGCTGATATGCCTCTTGGATGCACACTTTGTGTGTACATAGTTACCTTTAACTC 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ttctgctgctgctatgcctcttggatgcacactttgtgtgtacatagttacctttaact 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA107326 385 bp mRNA EST 04-FEB-1997 m195D10.r1 Stratagene mouse kidney (#937315) Mus musculus CDNA clone 519739 5' similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROFEIN ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 aatgattgccacaagn-aagaggatgcatctttcttcctggtgtacaagcctttaaagac 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 312;
                                                                                                                                                                                                                                                                                                                                                                                      2 others
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/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 0.00e+00;
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The Washu-HHMI Mouse EST Project
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Best Local Similarity 97.8%;
Matches 306; Conservative
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AA062853 312 bp mRNA EST 02-FEB-1997
zf70d09.rl Soares pineal gland N3HPG Homo sapiens cDNA clone 382289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1428 GGCACTGTTTTGGTGGAAGGCTTGGAGTTTTTTAATGAGTTTAGAGCTATTAGATAACC 1369
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Hillier., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rutaman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
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WashUn-Merck ESY Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                      Score 345; DB 30; Length 377;
Pred. No. 0.00e+00;
0; Mismatches 1; Indels
                                                                                                                                             /clone_lib="Soares pineal gland N3HpG"
/lab_host="DH10B (ampicillin resistant)"
complement(<1..>377)
14 c 74 g 116 t
                                                                                                                                                                                                                                                      ch 22.0%;
1 Similarity 99.2%;
358; Conservative
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Gaps ω ..

Indels

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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 414.
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Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrate; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 542)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollier,L., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Hitchi,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo./clone="682982"
                                                                                                                                                                                     Contact: Wilson RK Washindwerk Expression of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
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Pred. No. 4.47e-298;
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                                                                                                                                      The WashU-Merck EST Project
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308; Conservative
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                                                                                                                                                                                                                                                               ä
                                                                                                                             Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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2r90e08.rl Soares NbHTGBC Homo sapiens cDNA clone 682982 5'.
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91809443
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                                                                               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                  /clone="519739"
/clone_lib="Stratagene mouse kidney (#937315)"
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Pred. No. 0.00e+00;
0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                /sex="females"
/dev_stage="4 weeks"
/lab_host="SOLR (kanamycin resistant)"
                                Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 375.
Location/Qualifiers
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Best Local Similarity 84.2%;
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84°
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1..>385
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Gaps 13;

2; Indels 13; Length 542;

2 others

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1317 TCAGCAGCAGAA-GTCTTTAAAGGCTTGTAC-ACCAGG-AAGAAAG-ATGCATCCTC-TT 1263
                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampi
                                                                                        BP
                                                                                       standard; RNA; EST; 241
                             7.7%;
Local Similarity 99.2%;
les 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 241
                                                                                                                                                                                                                                                                   Unpublished.
                                                                                    HS368337
W20368;
q1296266
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                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        519
AA210789 542 bp mRNA EST 14-FEB-1997
zr90e08.rl Soares NbHTGBC Homo saplens CDNA clone 682982 5'
AA210789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels 13; Gaps
                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Pertebrata; Butheria; Primates; Catarrhini; Hominidae; Homo. [ bases 1 to 542] Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Palanan,M., Hultman,M., Kucaba,T., Le,M., Lebnon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcatattacatacatgtttatacataagcattacatttttttaataaaatgtatacagg
                                                                                                                                                                                   Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 229; DB 54; I
Pred. No. 4.47e-298;
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares NbHTGBC"
/tissue_type="Germinal B-cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                       WashU-Merck EST Project
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Similarity 95.4%;
30%; Conservative
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                                                                                                                                                                Unpublished (1995)
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                                                                    Homo sapiens
                                                                                                                                               Wilson, R.
                                     91809443
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Best Local S
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                  DEFINITION
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BASE COUNT
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JOURNAL
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                                              KEYWORDS
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normalization to a Cot = 5. Library constructed by M.Fatim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                      Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Barsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The WashU-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LIAL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 981 Std Error: 0.00 Seq primer: Ney Location/Qualifiers
05-MAY-1996 (Rel. 47, Created)
26-MAR-1997 (Rel. 51, Last updated, Version 2)
2668bll.s1 Soares fetal heart NbHH19W Homo sapiens CDNA clone
327453 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 241;
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                                                                                                                            Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib-"Soares fetal heart NDHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(<1..>241)
87 A; 40 C; 36 G; 76 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 120; DB 87; L
Pred. No. 2.15e-130;
0; Mismatches 0;
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Match 5.6%;
Local Similarity 66.5%;
les 208; Conservative
                                                                                                                                                                                      Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 119; DB 43; Length 501;
Pred. No. 6.68e-129;
0; Mismatches 26; Indels 10; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 gctgtatatgtatcgggtttcttcaaaggaaggacttcttttaaaggaaaggaaaagag 314
                                                                                                                                    Whitehead Institute/MIT Center for Genome Research; Physically
Mapped SISs
             31-MAY-1996
                                                                                                Bükaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
                                                                 human STSs derived from sequences in dbEST and the Uniqene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/map="188.1 cR from top of Chr5 linkage group"
23...151
                                                                                                                                                                                  Contact: Thomas Hudson Whitehead Institute/MIT Center for Genome Research Whitehead Institute/MIT Center Whitehead Institute for Blomedical Research 9 Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..... dbEST (genbank accession R45479).
Location/Qualifiers
1...501
                                                     STS sequence; primer; sequence tagged site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u
                                                                                                                                                                                                                                                                        Primer A: TATTCAGTATTGCCAAAATGAAGC
Primer B: TATTTTGAGTGTACAGATTAAGCA
STS size: 129
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                 0.025 units/ul
                                                                                                                                                                                                                                                    Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27..151)
117 g
                                                                                                                                                                                                                                                                                                                                Denaturation:
Annealing: 56 degrees C
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(127.
88 c 11
                                                                                                                                                                                                                                                                                                                                                                                              Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
                                                                                                                                                                                                                                                                                                                                                                PCR Cycles: 35
Thermal Cycler:
          G23282 501 bp
human STS WI-15758.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total Vol: 20 ul
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Best Local Similarity 84.9%;
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCl: 50 mM
Tris-HCL: 10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                 Tag Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Derived from dbEST
                                                                                                                                                                Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MgC12: 1.5 mM
                                                                                                                                                                                                                                                                                                                     Presoak:
                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pH: 9.3
                                                                           collection.
                                         91343608
                                                                                                                             Hudson, T
                                                                                                                                                                                                                                                                                                                                                                                      Protocol
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BASE COUNT
12
                  DEFINITION
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                                                                                     ORGANISM
                                                                                                                    REFERENCE
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                            caatcaccagccttggaagggcggcggggtgccgggggtgaggctggtttctaa 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ttcctttaatctgggcttgaggttaagttgcgacaacaggattgagttacttggggattg 181
                                                                                                                                                3 gagtecaactgtgaegteactecagtggtgtttgtagteagaeactegagaaaggee-ae 61
                                                                                                                                                                                                                                                                                                                                                   g1862038
06-MAR-1997 (Rel. 51, Created)
06-MAR-1997 (Rel. 51, Last updated, Version 1)
mx78g01.r1 Soares mouse NML Mus musculus cDNA clone 692496 5'
similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN
                                                                                                                435 ggggaaatggttgccacaggncagggggggggtgcctctttcntccggggggtacaggcttt 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contect: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108 Tel: 314 286 1800 Fax: 314 286 1810 Fax: 314 286 1810 Faxilis mousest@vatcon.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:426056 Possible Teversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson R.,
Waterston R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sequence 313 BP; 83 A; 58 C; 85 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="692496"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                             MM1155742 standard; RNA; EST; 313
AA237956;
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Gaps

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RESULT LOCUS

DEFINITION

ACCESSION KEYWORDS ORGANISM

REFERENCE AUTHORS

TITLE

COMMENT

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normalization to a Cot - 5. Library constructed by M.Fatim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHil9W."
/clone_127113"
/clone_lib="Soares fetal heart NbHH19W"
/sex-"unknown"
                                                                                                                                                                                                                 agaattttccgggttggaaggccaactggccttcttggatttcccct-caatcccttggc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ataaggagttetteatattggeattaatggagttggattttgaacagteteggttataga 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             801 ATATGTAGTATTCAATGTAACCATCGCTGCAGTTGATTTTTGACCAATCTGGATCACAAA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hiller L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Barsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The Washu-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK WashU-Merck EST Project Washington University Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 774 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 336.
                                                            gagtecaactgtgacgteactecagtggtgtttgtagteagaeactegagaaaggee-ae
                                                                                                                         1040 GAGTCCAGTCAACACATCGCTCCAGTGGTGTTTTATAATCAGAAACTCGAGAAAGGCCCAC
                                                                                                                                                                                          atataggaaaaagcaatgaggccaaactggagcaatggtcgtaagaagcctggccaatt
                                                                                                                                                                                                                                                                                                                   tteetttaatetgggettgaggttaagttgegacaacaggattgagttaettggggattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   861 AAGAGIGGCCIGAAIAGAAGGACAACCIGCCIICCIIAACICIIICIGCAIICCCICGAC
   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-WAY-1996 (Rel. 47, Created)
O7-WAR-1997 (Rel. 51, Last updated, Version 2)
zc64f09-11 Soares fetal heart NDHH19W Homo sapiens CDNA clone
327113 5' similar to WP:T28D9.3 CE02068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Indels
   Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; RNA; EST; 564
   ó
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             741 CATCCAAGAAGTG 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 gatgccagaaatg 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
   208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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HS942332
W30942;
g1311934
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA237956 313 bp mRNA EST 03-MAR-1997 mx78g01.rl Soares mouse NML Mus musculus CDNA clone 692496 5' similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i (bases 1 to 313)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
241 ataaggagttetteatattggeattaatggagttggatttgaacagteteggttataga 300
                                                                                                                         agaattttccgggttggaaggccaactggccttcttggatttcccct.caatcccttggc
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 57.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 313;
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Pred. No. 1.86e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo."
/clone="622496"
/clone_llb="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH108"
<1..>313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ų
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            מ
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:426056
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91862038
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source

FEATURES

BASE COUNT ORIGIN

mRNA

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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
anna <1..>564
Sequence 564 BP; 128 A; 155 C; 139 G; 134 T; 8 other;
   FT FT SO
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	.::	
	Gaps 2	
	2;	
Length 564;	Indels	
Score 76; DB 88;	Pred. No. 1.97e-66; 0; Mismatches 73	
watch 4.9%;	Best Local Similarity 67.8%; Pred. No. 1.97e-66; Matches 158; Conservative 0; Mismatches 73; Indels	
Ouery >	Best LK Matches	

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Search completed: Thu Nov 6 11:35:37 1997 Job time : 499 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Nov 4 10:23:32 1997; MasPar time 7.03 Seconds 498.122 Million cell updates/sec Run on:

Tabular output not generated.

Title:

Description: Perfect Score:

>0S-08-842-827-4 (1-285) from US08842827.pep 2119 1 MFDKTRLPYVALDVLCVLLA......HTTLHETPTTGNHYPSNHQP 285 Sequence:

PAM 150 Gap 11 Scoring table:

101610 segs, 12294212 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq28
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21

Mean 33.649; Variance 149.045; scale 0.226 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Mo. Score Mo. 109 109 109 109 109 109 109 109 109 109						
1 1009 2 1009 4 4 96 5 6 93 6 6 93 10 94 11 92 13 92 13 92	Ouery Match	Ouery Match Length DB	DB	a	Description	Pred. No.
2 109 4 4 105 5 4 93 6 6 93 7 7 94 10 94 11 91 13 92	5.1	193	77	W20304	H. pvlori cytoplasmic	1.86e+00
3 105 5 4 9 6 5 9 7 7 94 8 8 94 10 94 11 91 13 91	5.1	229	7	W20620	H. pylori cytoplasmic	1.86e+00
4 4 9 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	5.0	682	13	W04359	S. pneumoniae penicil	3.63e+00
5 6 7 7 9 9 9 9 11 12 9 9 13 9 9 9 9 9 9 9 9 9 9 9 9 9	4.5	397	18	W04217	Rat dorsal root gangl	1.58e+01
6 93 9 10 11 13 92 13 92 92	4.4	317	13	W02661	G-protein coupled hum	2.56e+01
7 8 9 10 11 12 13 92 13	4.4	317	16	R48689	G-protein coupled hum	2.56e+01
8 9 94 10 94 11 954 13 91	4.4	418	7	R39263	Human somatostatin re	2.18e+01
9 94 10 94 11 92 13 91	4.4	563	12	R53463	Pea proton transport	2.18e+01
10 94 11 92 12 91 13 92	4.4	1073	10	R55272	Alpha subunit of inte	2.18e+01
11 12 91 13 92	4.4	1073	Ŋ	R28821	Alpha 6A integrin sub	2.18e+01
12 91 13 92	4 .3	276	21	W20612	H. pylori protein.	3.00e+01
13 92	4.3	1091	'n	R28822	Alpha 6B integrin sub	3.51e+01
	4.3	1539	21	W13905	Human SMCY protein.	3.00e+01
14 91	4.3	3011	7	R34468	Encoded by full-lengt	3.51e+01
15 88	4.2	170	21	W20704	H. pylori transmembra	5.62e+01
16 90	4.2	205	21	W20268	H. pylori transporter	4.11e+01
17 89	4.2	250	9	R28365	Human LFA-3 protein.	4.81e+01
18 90	4.2	270	77	W20935	H. pylori transporter	4.11e+01
19 90	4.5	470	7	R34467	Encoded by Hepatitis	4.11e+01
20 90	4.2	470	^	R34476	Encoded by Hepatitis	4.11e+01

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Gaps

4

Score 109; DB 21; Length 193; Pred. No. 1.86e+00; 36; Mismatches 59; Indels 4

Query Match 5.1%; Best Local Similarity 20.8%; Matches 26; Conservative

	7.66e+01 8.93e+01
Encoded by Hepatitis H. pylori inner membr ABF-A from A. niger. Vitamin K dependent Rubella virus strain Human cardiac ogi PDE TATA-binding protein- Murine adenylate cycl Group I phospholipase Bovine phospholipase Low density lipoprote Low density lipoprote Low density lipoprote Novel mouse proteogly Human syndecan-1. Novel mouse proteogly Syndecan protein. 3-cylation enzyme. Murine somatostatin r Bacillus thuringiensi 6'-KD protein caryme. Murine somatostatin r Bacillus thuringiensi 6'-KD protein coxim. Infectious rubella vi	S. cerevisiae FKS1. A. rhizogenes NIAES17
F0F5H965F488606F0798945F	R72853 R42502
227 1100 1100 1100 1100 1100 1100 1100 1	8
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4444 4444 4444 4444 4444 4444 4444 4444 4444	4 4 5 4

ALIGNMENTS

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Tot. derivs. of bifunctional penicillin binding protein (BPBP) - opt. lack transglycosylase activity, useful to identify and assay for anthodies or cepts. Which bind BPBPs

Claim 2: Pages 65-68; lobgp: English.

Claim 2: Pages 65-68; lobgp: English.

The present sequence is a soluble variant of the S. pneumoniae penicillin binding protein (BPBP) 1A, which lacks the lst 38 amino acid residues of the wild type protein. Wild type PBP is a bifunctional protein, which binds the cell membrane when expressed or a bacterial cell, having transglycosylase and transpeptidase activities. The variant protein (NCIMB 4065) in conjunction with a labelled anti-lifunctional PBP monoclonal antibody, can be used to identify and assay for cpds. which bind bifunctional PBP. Such cpds., as lmbibitors of bifunctional PBP have a potential use in therapeutic cpds. which inhibit the growth of antibiotic resistant constraint. The soluble variant may also be used in X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 vynwdrgyf-gnitlgyalggsrnvpavetlnkvglnraktfl-nglgidypsihysnai 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-NOV-1996 (first entry)
Rat dorsal root ganglion P2x receptor.
ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist; antagonist; epilepsy; cognition; emesis; pain; asthma; peripheral vascular disease; hypertension; irritable bowel syndrome; premature ejaculation; cystitis; therapy.
03-DEC-1996 (first entry)

S. pnewmonlae penicillin binding protein 1A soluble variant.

Penicillin binding protein; PBP 1A; bifunctional protein;

transglycosylase; transpeptidase; identification; assay; inhibitor;

antibiotic resistant; bacteria; soluble variant; protein structure;

X-ray crystallography; determination.

Streptococus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| :||:| : |: | : | : | | || : | || : | : | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding ATP P2x receptors of the purinoceptor family - for screening opela. Useful in treating epilepsy, cognition, emesis, pain, asthma, peripheral vascular disease, hypertension, etc. Claim 1; Fig 3; 82pp; English.
The amino acid sequence (W04217) of rat dorsal root ganglion P2x Teceptor was deduced from a CDNA clone (T33854) isolated from a CDNA library. P2x receptors (see also W04215-16 and W04218) are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105; DB 19; Length 682
Pred. No. 3.63e+00;
20; Mismatches 22; Indels
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Best Local Similarity 28.6%;
Matches 18; Conservative
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24-MAY-1995; E01968.
27-MAY-1994; GB-010664.
09-FEB-1995; GB-002480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD.
Buell GN, Valera S;
                                                                                                                                                                                                                                                                                                                         29-JUN-1995; 013306.
01-JUL-1994; IN-000580.
24-NOV-1994; SE-004072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Town CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 96-042232/05.
N-PSDB; T08027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    682 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 96-030561/03.
N-PSDB; T33854.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASTR ) ASTRA AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Balganesh TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
WO9533048-A2.
                                                                                                                                                                                                                                                                                                 10-JAN-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Particological polypertical acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter claim 61: Page 1047: 1481pp; English.

This sequence represents a H. pylori cytoplasmic protein.

This sequence represents a H. pylori polypeptide blinding compounds, useful as potential H. pylori polypeptide blinding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori 16 cycle activators or inhibitors.

The genomic sequence of H. pylori farct 55679) was determined from cyclings generated by mechanically shearing the bacterial DNA. The sequence of H. pylori for ONE of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To dentify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 eeidalalefgaii-eqklfdrghlnsevmafidkhyqnyifhiasaalhselqvlcefl 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ILV-GVGLPVSSIILGETLSVYCNLL-HSNSFISNNYIATIYKAIGTFLFGAAASQS-LT 117
                                                                                                                                                                             74 eeidalaalefgaii-eqklfdrghlnsevmafidkhyqnyifhiasaalhselqvlcefl 132
                                                                                                                                                                                                                            21 ifdsmhlkyegfkalfqkhgndskeglkqfevyhyqsggisrnekiqyfyneilktplaq 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MFDKTRLPYVALDVLCVLLASMPMAVIKLGQIYPFQRGFFCKDNSINYPYHDSTAASTVL 60
                                  14 ifdsmhlkyegfkalfqkhgndskeglkqfevyhyqsggisrnekigyfyneilktpiaq 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109; DB 21; Length 229;
Pred. No. 1.86e+00;
36; Mismatches 59; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-1997 (first entry)
14-JUL-1997 (first entry)
Lylori cytoplasmic protein, OžaellGilorf5.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith D, Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W04359 standard; Protein; 682 AA. W04359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.1%;
Best Local Similarity 20.8%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-1996, 009122.
06-JUN-1995; US-487032.
01-APR-1996; US-630405.
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WO9640893-A1.
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Berglindh OT, Smit
WPI; 97-052306/05.
                                                                                                                                                                                                                                                                                                                         133 g1tky 137
                                                                                                                                                                                                                                                                                                                                                                                              118 DIAKY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T67873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 gitky 144
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Length 682;

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US-943236.
    09-SEP-1993;
                     10-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The W dopamine receptor peptide - useful as antipsychotic agent, e.g.

To treating schizophrenia

For treating schizophrenia

Disclosure; Column 49-51; 184pp; English.

Enforced R W0257-W02720 represent a range of G-protein coupled receptor

CGPR) proteins welected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endochelin, bombesin, endocrine, rhodopsin, opsin, adrenergic, thrombin, endochelin, bombesin, endocrine, rhodopsin, opsin, cadrant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays.

The polypeptide fragments retain biological activity such as binding GPR ligand or modulating GPR ligand binding to a GPR (see W02747-W02999) for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects such as pathology related to a GPR abnormality e.g. a psychotic disorder such as
                                                                                                                                                       ij
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                                                                                                                                                                                                                                                                                                        12-NOV-1996 (first entry)
G-protein coupled human m2 muscarinic acetylcholine receptor.
G-protein coupled receptor; ligand binding assay; transmembrane domain; schizoptenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1996 (first entry)
G-protein coupled human m2 muscarinic acetylcholine receptor protein.
G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus.
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
             ATP. Recombinant Pox receptors can be produced in prokaryotic or eukaryotic, pref. mammalian, host cells. Their widespread distr. throughout the body and possibly numerous physiological roles make P2x receptors useful for the screening of new cpds. (agonists or antagonists) for the treatment of a number of pathological states. Sequence 397 AA;
 ligand-gated ion channels that open upon binding of extracellular
                                                                                                                                                       ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DB 19; Length 317; Pred. No. 2.56e+01;
                                                                                                                         Length 397;
                                                                                                                      Score 96; DB 18; Length 397
Pred. No. 1.58e+01;
14; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 vvcdlyvvsnasvmnl-liisfdr-yfcvtkpltypvkrttkmagmmi 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tvlcdiillnflkgadhykarkfeevtettlkgtastnpvfasdq 380
                                                                                                                                                                                                   240 AILVAVYVSDFFKERTSFKERK-EEDSHTTLHETPTTGNHYPSNH 283
                                                                                                                                                                                                                                                                            W02661 standard; peptide; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 6
R48689 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1996.
10-SEP-1992. 943336.
10-SEP-1992: US-943236.
09-SEP-1993: US-118270.
(UVN ) UNIV NEW YORK STATE.
MUTPHY RB. SCHISTER DI;
WPI: 96-208785/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 29.2%;
Matches 14; Conservative
                                                                                                                      Query Match
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens.
WO9405695-A1.
17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                      Homo saptens.
USS508384-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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The sequences given in R39259, R39261 and R39263 represent the human sometostatin receptors (SSTR)-1, SSTR-2 and SSTR-3. The DNA encoding these procebins was isolated from total human pancreatic islet DNA. These procebing was lacolated from total human pancreatic islet DNA. These DNA sequences may be placed under the control of a suitable promoter and used to transform a host cell. The DNA sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    these proteins may be used in screening assays for testing candidates including agonists and anteaponists of SSTR polypeptides. The assays may be used to discriminate candidate substances with desirable properties specific to SSTR polypeptides. The isolated substances may be used in a wide range of aplications eg. diagnosis of various human tumours. Fragments of these DNA sequences may be used as probes in the isolation of other SSTR-encoding clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                      Polypeptides of G-coupled receptor proteins (GPRs) - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; somatostatin; receptor; SSTR-1; SSTR-2; SSTR-3; tumour;
pancreas; islet; promoter; transformation; host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 34.9%; Score 94; DB 7; Length 418; Local Similarity 34.9%; Pred. No. 2.18e+01; nes 22; Conservative 17. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 vvcdlyvvsnasvmnl-liisfdr-yfcvtkpltypvkrttkmagmmi 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R39263 standard; Protein; 418 AA.
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(UYNY ) UNIV NEW YORK STATE.
Murphy RB, Schuster DI;
WPI; 94-101120/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
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WPI; 93-227272/28.
N-PSDB; 045657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1992; Ull327
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01-OCT-1990; US-591105
                                                                                                           N-PSDB; 065673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 YCMLEVALYLQARMKGDWARLLRPT-LQFGLVAVS-IYVGLSRVSDYKHHWSDVL-TGLI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.18e+01;
20; Mismatches 31; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1995 (first entry)

Apphs subunit of integrin cell surface receptor.

Integrin; alpha; beta; subunit; glycoprotein; heterodimer;

transmembrane; extracellular matrix; cell signalling; cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                    Proton transport adenosine tri.phosphatase protein and its coding gene - for preparation of pure proton transport adenosine tri:phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 6-7; 8pp; Japanese.
This sequence is a proton transport adenosine triphosphatase protein from the plasma membrane of Pisum sativum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.4%; Score 94; DB 10; Length 563;
Best Local Similarity 27.0%; Pred. No. 2.18e+01;
Matches 20; Conservative 20; Mismatches 31: Indale
                                                                                                                                                                                     Pea proton transport adenosine triphosphatase.
Proton transport adenosine triphosphatase; H+ATPase; pea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= f
/note= "This sequence is conserved in all but the
Drosophila PS2 alpha subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_binding 230..238
/note= "Sequence weakly homologous with cation binding site of other integrin alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note "This sequence closely resembles the cleavage site of other integrin 0 chains." misc_feature 1040 .1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            behaviour; signal transduction; receptor Romo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_binding 324..332
/note= "putative cation binding site."
misc_binding 386..394
/note= "Putative cation binding site."
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/note= "Putative cation binding site."
misc_feature 899..903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T ' 9
R55272 standard; Protein; 1073 AA.
                                                                                                                         R53463 standard; Protein; 563 AA.
                                                                                                                                                                                                                                                                                      29-SEP-1992; 260333.
29-SEP-1992; JP-260333.
(YAMH) NIPPON STEEL CHEM CO.
(YAMA) NIPPON STEEL CORP.
WPI; 94-172755/21.
                                                                                                                                                               18-JAN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 vaqliatliavyas 491
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19-FEB-1987; 016552.
19-FEB-1987; US-016552.
04-JAN-1989; US-293384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 AA;
                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q63601.
                                                                                                                                                                                                                                  Pisum sativum.
                                      107 LFG 109
                                                                                                                                                                                                                                                    J06113862-A.
94 mlg 96
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                                                                                                                                               R53463;
                                                                                                     NAME OF THE STATE 
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23; Mismatches 29; Indels 7; Gaps 7;
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                                                                                                                                                                                                                                               are non-covalently associated transmembrane glycoprotesins. Il alpha chains and 6 beta chains have been recognised in man. Each alpha subunit tends to associated transmembrane glycoprotesins. Il alpha subunit tends to associate with only one type of beta subunit but there are several exceptions. Integrins mediate (in part) the interaction of calls with the extracellular matrix, forming a link between the extracellular matrix and the cytoskeleton. They may transmit signals from the extracellular to the intracellular subunit of an alpha6 beta4 integrin. This sequence is the alpha6 sequence 1073 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha 6A integrin subunit.

Human; alpha 6A; alpha 6B; integrin; cell surface receptor; adhesion; extracellular matrix; cytoskeleton; heterodimer; laminin receptor; immunoprecipitation; JAR; choriocarcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing presence of abnormal epithelial tissue in vitro - utilises monoclonal antibodies to alpha6 beta4 cell surface protein Example 5; Figure 6; 34pp; English. Integrins are heterodimers comfised of alpha and beta subunits, that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 94; DB 10; Length 1073; Pred. No. 2.18e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binding_site 230..238
/note= Putative cation binding domain"
Binding_site 324..332
/note= Putative cation binding domain"
Binding_site 386..394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R28821 standard; Protein; 1073 AA
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/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 SHTT-LHETPTTGNHYPSN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.3%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label Glycosylation_site
Modified_site 731
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ied_site 748
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Modified_site 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-1993 (first entry)
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Protein 24.,1073
/label Mature protein
                                                       Quaranta V;
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                           QUARANTA V.
                                                       Kajiji S, Quarante
WPI; 94-191533/23.
(KAJI/) KAJIJI S.
(QUAR/) QUARANTA '
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12-NOV-1992
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The sequences given in R28821-22 are the human alpha 6A and 6B
The sequences given in R28821-22 are the human alpha 6A and 6B
The sequences given in R28821-22 are the human alpha 6A and 6B
Thegrin subulits. Integrins are a family of cell surface receptors
which serve cellular adhesion functions. These receptors form a link
between the extracellular matrix and the cytoskeleton through their
changes to various extracellular components. Each integrin receptor
is a heterodimer comprised of an alpha and a beta subunit. Each alpha
subunit tends to associate with only one type of beta subunit but
there are several exceptions to this rule. These integrins correspond
to the laminin receptor. The cytoplasmic domain of the 6A and 6B
integrins differs from previously isolated alpha 6 integrins. The
changes alpha 6B was isolated from human choriocarcinoma cell line JAR
Sequence 1073 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   997 vrvtvípskt-vagysgvpwwiilvailagilmlallvíilwkcgffk-rnk-kdhydat 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 VAVSIYVGLSRVSDYK-HHWSDVLTGLIQGALV-AILVAV-YVSDFFKERTSFKERKEED 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 5; Length 1073;
Pred. No. 2.18e+01;
23; Mismatches 29; Indels 7; Gaps
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                                                                                                                                                                                                                                                                                                                                        Integrin alpha sub-unit cytoplasmic domain polypeptide(s) - used for prodn. of antibodies and in detection of integrin sub-units
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding compound; bacterium; life cycle, activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; prevention; treatment; infection; identification;
                                                                                           /label- Cytoplasmic_domain
/note- "Conservered in virtually all integrins"
  "Putative cation binding domain"
                       Binding_site 441..449
/note- "Putative cation binding domain"
Domain
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06-UUN-1995. U09122.
07-UUN-1995. US-487032.
01-APR-1996; US-630405.
(ASTR ) ASTRA AB.
BEETJINGH OT. Smith D, Mellgaerd BL;
WPI: 97-052306/08.
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Local Similarity 25.3%;
hes 20; Conservative
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                                                                                                                                                                  12-NOV-1992,
27-APR-1992, U03527.
03-MAY-1991; US-695564.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                 Quaranta V, Tamura RN;
WPI; 92-398799/48.
N-PSDB; Q31188.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori protein.
                                                                                                                                                                                                                                                                                                                                                                                       in body samples
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                                                                                                                                        409219647-A.
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Alpha 6B integrin subunit:
Muman, alpha 6A; alpha 6B; integrin; cell surface receptor; adhesion;
extracellular matrix; cytoskeleton; heterodimer; laminin receptor;
immunoprecipitation; JAR; choriocarcinoma.
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                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. Pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from production, p.g. in E. coli hosts.
                                                                                                                                                                                                                                                        Score 92; DB 21; Length 276; Pred. No. 3.00e+01; 21; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note- "Conservered in virtually all integrins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Position of deletion of alpha 6A"
W09219647-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding_site 230.238
/note= "Putative cation binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding_site 324..334
/note= "Putative cation binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding_site 386..394
/note= "Putative cation binding domain"
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/note= "Putative cation binding domain"
1040..1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                        Query Match 4.3%;
Best Local Similarity 24.7%;
Matches 18; Conservative
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/label= Glycosylation_site
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/label= Glycosylation_site
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/label= Glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified_site 891
/label- Glycosylation_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label = Glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- Glycosylation_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label = Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label - Mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 WSKINCSDGYIEY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified_site
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The sequences given in R2881-22 are the human alpha 6A and 6B integrins subunits. Integrins are a family of cell surface receptors which serve cellular adhesion functions. These receptors form a link between the extracellular matrix and the cytoskeleton through their between the extracellular matrix and the cytoskeleton through their is a heterodimer comprised of an alpha and a beta subunit. Each alpha subunit tender comprised of an alpha and a beta subunit. Each alpha there are several exceptions to this rule. These integrins correspond to the laminin receptor. The cytoplasmic domain of the 6A and 6B integrins differs from previously isolated alpha 6 integrins. The human alpha 6B was isolated from human choriocarcinoma cell line JAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D NOT CONTROL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       997 vrvtvípskt-vagysgvpwwiilvailagilmlallvíilwkcgíík-rsrydd 1049
                                                                                                                                                                                                                           N-PSDB; Q31189.
Integrin alpha sub-unit cytoplasmic domain polypeptide(s) - used for prodn. of antibodies and in detection of integrin sub-units in body samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 VAVSIXVGLSRVSDYK-HHWSDVLTGLIQGALV-AILVAV-YVSDFFKERTSFKE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMCY; Y chromosome; male fertility; sex determination; H-Y antig
minor histocompatability antigen; male contraceptive; evolution;
embryogenesis; spermatogenesis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 4.3%; Score 92; DB 21; Length 1539; Best Local Similarity 26.2%; Pred. No. 3.00e+01; Matches 11; Conservative 12; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 91; DB 5; Length 1091;
Pred. No. 3.51e+01;
17; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J 13
W13905 standard; Protein; 1539 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // Match
Local Similarity 27.3%;
hes 15; Conservative
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10-JUN-1997 (first entry)
                                                                                              (SCRI ) SCRIPPS RES INST.
                                                 US-695564
                                                                                                                                                Ouaranta V, Tamura RN;
WPI; 92-398799/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1539 AA:
    27-APR-1992; U03527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1091 AA
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WO9710267-A1.
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N-PSDB; 040426.

DNA and CDNA of hepatitis C virus • useful as probes for diagnosing HCV inhead to the claim 3: Page 6-18: 44pp; Japanese.

CDNA was prepared from HCV genomic RNA. Full-length clone JK1-B and 14 shorter clones were isolated by PCR amplification.

Primer/probes derived from the sequences of these clones can be used in diagnostic assays for HCV. See also Q40425-Q40439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1997 (first entry)
H. pylori transmembrane protein, OSapil505orf10.
H. pylori transmembrane protein, Treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.3%; Score 91; DB 7; Length 3011; Best Local Similarity 35.5%; Pred. No. 3.51e+01;
                                                                                                                                                                                                                                                  liver disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches 10; Indels
                                                                                                                                                                                30-JUL-1993 (first entry) Encoded by full-length Hepatitis C virus clone JKI-B. Encoded by full-length Hepatitis virus; NANBHV; liver dise Polymerase chain reaction; diagnostic method.
141 KINCSDGYIEYYICRGNAERVKEGRLSFYSG-HSSFSMYCML 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 mvgnwakvlivmllfagvdgttyvsvghasg 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                            Location/Qualiflers
                                                                                            r 14
R34468 standard; Protein; 3011 AA.
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30-MAY-1991; JP-153736.
(SANW ) SANWA KAGAKU KENKYUSHO CO.
WPI; 93-130638/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W20704 standard; Protein; 170 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berglindh OT, Smith D, WPI; 97-052306/05.
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                      Misc_difference 2414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori. WO9640893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "not defined"
J05068562-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3011 AA
                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
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                                                                                                                                                        R34468;
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The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant

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Gaps

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304 knhssaqfidsyicqvcsrgdednkllfcdgcddnyhifell 345

Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter Claim 73; Page 1122, 1461 Helicopacter Claim 73; Page 1122, 1461 Helicopacter Protein likely to contain four this sequence represents a H. pylori protein likely to contain four

N-PSDB; T67957

membrane spanning regions.

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homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polymeptide
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9
Gaps
9;
ngth 170; Indels
L; 20;
Score 88; DB 21; Pred. No. 5.62e+0. 19; Mismatches
Ouery Match 4.2%; Score 88; DB 21; Length 170; Best Local Similarity 31.8%; Pred. No. 5.62e+01; Matches 21; Conservative 19; Mismatches 20; Indels 6; Gaps 6;
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Nov 4 10:21:54 1997; MasPar time 10.95 Seconds 751.945 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score: Sequence:

>US-08-842-827-4 (1-285) from US08842827.pep 2119 1 MFDKTRLPYVALDVLCVLLA......HTTLHETPTTGNHYPSNHQP 285

PAM 150 Gap 11 Scoring table:

91006 segs, 28888923 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 46.052; Variance 108.101; scale 0.426 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No	2.63e-12	1,35e-10	1.11e-02	3.31e-02	1.65e-01	7.82e-01	6.06e-01	7.82e-01	7.82e-01	7.82e-01	1.01e+00	3.50e+00	2.74e+00	3.50e+00	3.50e+00	3.50e+00	2.74e+00	2.74e+00	2.74e+00	2.74e+00	2.74e+00
Description	hypothetical protein		NADH dehydrogenase (hypothetical protein	penicillin-binding p	hypothetical protein	NADH dehydrogenase (penicillin-binding p	penicillin-binding p	penicillin-binding p	cycloheximide resist	probable olfactory r	hypothetical protein	NADH dehydrogenase (NADH dehydrogenase (linoleoyl-CoA desatu	penicillin-binding p	penicillin-binding p	penicillin-binding p	penicillin-binding p	genome polyprotein -
8	569561	S70114	QXXL2M	S32217	S28036	S15308	S28760	528037	A42893	528038	JC1173	S58012	138164	568129	B34284	S54809	\$28034	528031	S28033	S28032	GNWVDP
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& Query Match	9.1	8.5	5.7	5.5	2.5	5.0	5.0	5.0	5.0	5.0	4.9	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7
Score	193	181	121	117	111	105	106	105	105	105	104	66	100	66	66	66	100	100	100	100	100
Result No.	1	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21

155244 adenosinetriphosphat 4.47e+00 510188 NADH dehydrogenase (5.70e+00 554413 hypothetical protein 5.70e+00 554550 cyck protein - Rhizo 4.47e+00 H4.74-transporting A 5.70e+00 625517 nonstructural protein 5.70e+00 637445 denome polyprotein - 4.47e+00 6NWV16 genome polyprotein - 4.47e+00 6NWV26 genome polyprotein - 4.7e+00 6NWV26 genome polyprotein - 4.7e+00 6NWV26 polyprotein - 6ngue 5.70e+00 6NADH dehydrogenase (7.25e+00	ALIGNMENTS pe complete rotein YDR503c - yeast (Saccharomyces accharomyces cerevisiae equence_revision 06-Sep-1996 #text_change he EMBL Data Library, August 1995 of S. cerevisiae cosmids 8166, 9787, 9717, and abel DIE molecular-weight 31586 #checksum 1196	3; DB 11; Length 274; 2.63e-12; matches 56; Indels 9; liignlrpdfvdrcipdlqkmsdadsl-
4.6 346 10 4 4.6 4.6 3.6 10 4.6 5.6 5.6 5.6 5.6 5.6 5.6 5.6 5.6 5.6 5	S69561 #ty hypothetical proportical acerevisiae) #formal_name S 22-Aug 1996 #s 0 6 569 51	nilarity 35.1% Conservative -hfmhtsilclmlili ITTINAIGFLFGA KQtnkwillyeglkst STONAERV - EGRLSF WWSTVIGHTHWSD WWSTVIGHTHWSD WGLSRVSDYKHHWSD S70114 #t hypothetical Cerevisiae) #formal_name 24-Aug-1996 66-Sep-1996
	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE # authors on # description # accession # acces	Matc Matc

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16;
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membrane-associated complex; mitochondrion; NAD; oxidative
phosphorylation; oxidoreductase; respiratory chain
#length 345 #molecular-weight 37671 #checksum 3982
                                                                                                                                                                                                                                                                                                                                                                                                             96 lytsligisi-aw-f--sts-fftnfiknwigrlrpdfldrcqpv-eglpldtlftakdv 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OXXL2M #type complete
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2
African clawed frog mitochondrion (SGC1)
Africanione oxidoreductase chain 2
#formal_name mitochondrion Xenopus laevis #common_name
African clawed frog
28-reb-1986 #sequence_revision 28-reb-1986 #text_change
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Roe, B.A.; Ma, D.P.; Wilson, R.K.; Wong, J.F.H.
#journal J. Biol. Chem. (1985) 260:9759-9774
#title The complete nucleotide sequence of the Xenopus laevis
#cross-references MUID:85261388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #length 289 #molecular-weight 33514 #checksum 4703
                                                                                                                                                                                                                                                                                             62; Mismatches 98; Indels 18;
                                                                                                                                                                                                                                                         Score 181; DB 11; Length 289
Pred. No. 1.35e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.7%; Score 121; DB 1; Length 345; Best Local Similarity 25.3%; Pred. No. 1.11e-02; Matches 21; Conservative 27; Mismatches 28; Indels
                $70114
Fulton, L.
submitted to the EMBL Data Library, May 1996
The sequence of S. cerevisiae cosmid 9819.
$70114
                                                                                                                                       1-289 ##label FUL
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Best Local Similarity 27.6%;
Matches 68; Conservative
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Rauschenbach, R.; Isernhagen, M.; Noeske-Jungblut, C.;
Boddol, W.; Siewert, G.
submitted to the EMBL Data Library, March 1993
Cloning, sequencing and expression of the gene for cytochr
P450meg, the steroid 15beta-monooxygenase from Bacillus
megaterium ATCC 13368.
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EMBO J. (1992) 11:3831-3836
Relatedness of penicillin-binding protein la genes from
different clones of penicillin-resistant Streptococcus
pneumoniae isolated in South Africa and Spain.
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Y #length 216 #molecular-weight 24946 #checksum 8213
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Pred. No. 3.31e-02;
31; Mismatches 37; Indels
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Best Local Similarity 30.2%; Pred. No. 1.65e-01;
Matches 19; Conservative 19; Mismatches 22;
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                108 lapf-hfwlpevlqglslttgli 129
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Best Local Similarity 29.4%;
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##residues 1-77
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   Jiang, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana,
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Genetics (1992) 131:397-412
A novel mitochondrial genome organization for the blue
mussel, Mytilus edulis.
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phosphorylation; oxidoreductase; respiratory chain
#length 441 #checksum 3300
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Pred. No. 7.82e-01;
14; Mismatches 27; Indels
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Pred. No. 6.06e-01;
25; Mismatches 28; Indels
                                                                                                                            #journal Mol. Microbiol. (1991) 5:695-713
#title Structure and sequence of the rfb (0 antigen)
#cross-references MUID:91260454
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Best Local Similarity 31.1%;
Matches 19; Conservative
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Best Local Similarity 28.8%;
Matches 23; Conservative
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J. Bacteriol. (1992) 174:4517-4523
Nucleotide sequences of genes encoding penicillin-binding proteins from Streptococcus pneumoniae and Streptococcus oralis with high homology to Escherichia coli
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$28037 *type fragment
penicillin-binding protein la - Streptococcus pneumoniae
(strain 63915) (fragment)
#formal name Streptococcus pneumoniae
17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change
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Martin, C.; Sibold, C.; Hakenbeck, R.

EMBO J. (1992) 11:3831-3836

Relatedness of penicillin-binding protein la genes from different clones of penicillin-resistant Streptococcus pneumoniae isolated in South Africa and Spain.
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penicillin-binding protein 1A - Streptococcus pneumoniae
*formal_name Streptococcus pneumoniae
07.Apr-1994 *sequence_revision 07.Apr-1994 *text_change
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Pred. No. 7.82e-01;
20; Mismatches 22; Indels
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#cross-references FB:M90527
# #length 719 #molecular-weight 79701
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X #length 719 #checksum 2230
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Januska, A.; Janulaitis, A.
#journal Gene (1992) 116:105-108
#title Cloning and sequence analysis of a Candida maltosa gene which confers resistance to cycloheximide.
#cross-references_MUID:92331941
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14.5cmal_lamme Homo sapiens #common_name man
13.4an-1996 #sequence_revision 19.Apr-1996 #text_change
19.Apr-1996
SS5012
SS7995
Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.
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                              Martin, C.; Sibold, C.; Hakenbeck, R. Martin, C.; Sibold, C.; Hakenbeck, R. EMBO, 7. (1992) 11:3811-3836 Relatedness of penicillin-binding protein la genes from different clones of penicillin-resistant Streptococcus pneumoniae isolated in South Africa and Spain.
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#length 552 #molecular-weight 61400 #checksum 9303
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4.9%; Score 104; DB 11; Length 552;
Best Local Similarity 25.7%; Pred. No. 1.01e+00;
Matches 18; Conservative 29; Mismatches 17; Indels
                                                                                                                                                                                                                                                                  Length 719;
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                                                                                                                                                                                                                                                              Score 105; DB 10;
Pred. No. 7.82e-01;
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##residues
##cross-references EMBL:X67873
'Y #length 719 #checksum 2709
                                                                                                                                                          translation not shown
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                                                                                                                                                                                                                                                          Query Match 5.0%;
Best Local Similarity 28.6%;
Matches 18; Conservative
18-Nov-1994
S28038
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##residues 1-7
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117 TDIAKYSIGR 126
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#authors Crouzet, J.; Levy-Schil, S.; Cameron, B.; Cauchois, L.;
Rigault, S.; Rouyez, M.C.; Blanche, F.; Debussche, L.;
Thibaut, D.
J. Bacteriol. (1991) 173:6074-6087

*title J. Lactobase-pair Pseudomonas denitrificans DNA fragment containing five cob genes and identification of structural genes encoding cob(I)alamin adenosyltransferase, cobyric acid synthase, and bifunctional cobinamide kinase-cobinamide phosphate guanylyltransferase.

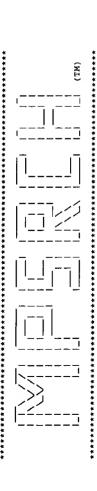
#cross-references MUD:92011366

#accession 138164
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*submission submitted to the EMBL Data Library, July 1995
*description Male germ cells from several mammallan species express a
specific repertoire of olfactory receptor genes.
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NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 -
Protopterus dollol mitochondrion (SGC1)
*formal_name mitochondrion Protopterus dollol
66-Dec-1996 *sequence_revision 06-Dec-1996 *text_change
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hypochetical protein 9 - Pseudomonas sp.
hypochetical protein 9 - Pseudomonas sp.
31-Jul-1992 #sequence_revision 31-Jul-1992 #text_change
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:X #length 261 #molecular-weight 27374 #checksum 9744
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4.7%; Score 100; DB 8; Length 261;
Best Local Similarity 31.1%; Pred. No. 2.74e+00;
Matches 19; Conservative 18; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                           Score 99; DB 13; Length 157;
                                                                                                                                                                                                                                                                                                                                                                   26; Mismatches 31; Indels
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Genetics (1996) 142:1249-1263
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Y #length 157 #checksum 7167
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                                                                                                     ##molecule_type mRNA
##residues
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Best Local Similarity 28.3%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-Dec-1996
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B34284 *type complete
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - sea
urchin (Paracentrotus lividus) mitochondrion (SGC8)
#formal_name mitochondrion Paracentrotus lividus #common_name
common urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gadaleta, M.N.; Saccone, C.
Gene (1987) 53:41-54
A novel gene order in the Paracentrotus lividus mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the authors translated the nucleotide sequence using the standard genetic code; the authors translation is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 134-135,'M',137-148,'K',150-154,'K',156-183,'M',185-189,
'M',191-193;202-211,'K',213-223,'M',225-230,'K',
232-238,'M',240,'M',242-247,'M',249-263 ##label CA2
##cross-references GB:M16516
The complete nucleotide sequence of the mitochondrial genome of the lungfish (Protopterus dolloi) supports its phylogenetic position as a close relative of land vertebrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. (1989) 264:10965-10975
The complete nucleotide sequence, gene organization, and genetic code of the mitochondrial genome of Paracentrotus lividus.
                                                                                                                                                                                                                                                                                       51 rateaatkyflagaaasim-ilfssm-inawvagewnitnlisptsa-tlitlalaikig 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cantatore, P.; Roberti, M.; Rainaidi, G.; Gadaleta, M.N.;
Saccone, C.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-Jun-1990 #sequence_revision 29-Jun-1990 #text_change 04-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cantatore, P.; Roberti, M.; Morisco, P.; Rainaldi, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #Superfamily NADH dehydrogenase (ubiquinone) chain 2
membrane-associated complex; mitochondrion; NAD;
oxidoreductaes
#length 352 #molecular-weight 39009 #checksum 8650
                                                                                                 Score 99; DB 5; Length 352;
Pred. No. 3.50e+00;
22; Mismatches 26; Indels 10;
                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                       DB 16; Length 342;
                                                                                                                                                                                                                           Pred. No. 3.50e+00;
32; Mismatches 25; Indels
                                                                                                                                                                                                     Query Match

4.7%; Score 99;
Best Local Similarity 25.0%; Pred. No.
Matches 22; Conservative 32; Misma
                                                                                                                                                                                                                                                                                                                                                                       108 -lap-mhfwlpevlqgvtlmt-gailvt 132
                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type_DNA
##residues 1-352 ##label CAN
##cross-references GB:J04815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *cross-references MUID:89291831
*accession B34284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:87248108
#accession A26510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.7%;
Best Local Similarity 32.6%;
Matches 28; Conservative
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mitochondrion
SGC8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A26510
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                                                                                    *accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
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  #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Nov 4 10:20:41 1997; MasPar time 7.75 Seconds 780.375 Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-08-842-827-4 (1-285) from USO8842827.pep 2119 1 MFDKTRLPYVALDVLCVLLA......HTTLHETPTTGNHYPSNHQP 285

59021 seqs, 21210388 residues Searched:

PAM 150 Gap 11

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 47.899; Variance 90.096; scale 0.532 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SITMMARTES

perd		7.00e-67	6.87e-04	1.16e-01	8.52e-02	1.16e-01	1.57e-01	3.86e-01	5.19e-01	6.96e-01	5.19e-01	1.24e+00	1.24e+00	9.31e-01	9.31e-01	1.24e+00	9.31e-01	9.31e-01	1.24e+00	2.20e+00	2.20e+00	1.66e+00	1.66e+00
Description		HYPOTHETICAL 39.0 KD	NADH-UBIQUINONE OXIDO	RFBX PROTEIN.	NADH-UBIQUINONE OXIDO	PENICILLIN-BINDING PR	CYCLOHEXIMIDE RESISTA	PUTATIVE MITOCHONDRIA	HYPOTHETICAL 27.4 KD	NADH-UBIQUINONE OXIDO	GENOME POLYPROTEIN (C	NADH-UBIQUINONE OXIDO	STRUCTURAL PROTEIN MD	CYTOCHROME C-TYPE BIO	PLASMA MEMBRANE ATPAS	PROBABLE CADMIUM-TRAN	GENOME POLYPROTEIN (C	GENOME POLYPROTEIN (C	GENOME POLYPROTEIN (C	HYPOTHETICAL PROTEIN	NADH-UBIQUINONE OXIDO	NADH-UBIQUINONE OXIDO	NADH-UBIQUINONE OXIDO
SUMMARIES		YSX3_CAEEL	NU 2M_XENLA	RFBX_SALTY	NUSM_MYTED	PBPA_STRPN	CYHR_CANMA	YDE9_SCHPO	YCB9_PSEDE	NU2M_PARLI	POLG_DEN2P	NU2M_CHICK	MDM1_YEAST	CCMF_RHIME	PMA2_LYCES	CADA_BACFI	POLG_DEN26	POLG_DEN27	POLG_DEN2N	YIAM_HAEIN	NU2M_COTJA	NU2M_PHOVI	NU2M_HALGR
DB	;	7	7	ω	7	7	m	11	1	^	7	o	ø	~	~	7	^	~	7	디	9	۲	7
Length DB		341	345	430	522	719	552	345	261	352	3388	346	443	9/9	704	723	3391	3391	3391	161	346	347	347
e Ouery Match		21.4	5.7	5.0	5.0	5.0	4.9	4.8	4.7	4.7	4.7	4.6	4.6	4.6	9.	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.5
Score		454	121	105	106	105	104	101	100	66	100	97	97	86	86	97	98	86	97	95	92	96	96
Result No.		п	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	50	21	22

qarlgpvlnnrivvpisqtlmfmiglgisfsritdnkhhwsdvlvgifigiflavytctf 272

213

94 yrmqkvesni-nnpryrwrnnhlhvlfvrlltyfgysqigfvmnialnivtkhvvgrlrp 152

34 flataavtvivptllgvsgrgffcdddsiryeyrkdtitavglmlynlvlnaatvlfvey 93

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PAY3_RAT NONSTRUCTORAL PROTEIN 1.66e+00 NONSTRUCTORAL PROTEIN 2.20e+00 ELYCOPROTEIN 047 PREC 2.20e+00 SSR3_HUWAN SOMATOSTAIN RECEPTOR 2.91e+00 NATOC_SCHPO PROBABLE CADMIUM-TRAN 2.91e+00 PAM2_RATH PROTEIN 1.66e+00 PAM3_RARTH PROTEIN PROTEIN 2.91e+00 PAM3_RARTH PROTEIN FOR 5.01e+00 INMO_ECOLI IMMUNITY PROTEIN FOR 5.08e+00 ATPS_ECOLI PROSEIN (1245). CHIL_ARATH NETFCHIORATE TRAN 5.08e+00 NUTSM_POND NATH-TICAL 61.2 KD 6.68e+00 NUTSM_POND NATH-TICAL 61.2 KD 6.68e+00 NUTSM_POND NATH-TICAL 61.2 KD 7.60e+00 NUTSM_STREN HYPOTHETICAL 61.2 KD 7.60e+00 NUTSM_POND NATH-TICAL 61.2 KD 7.60e+00 NUTSM_POND NATH-TICAL 61.2 KD 7.60e+00 NUTSM_POND NATH-TICAL 61.2 KD 7.60e+00 NUTSM_STREN NATH-TICA	341 AA. 341 AA. E UPDATE) 10N UPDATE) 1.3 IN CHROMOSOME II. IEMATODA; SECERNENTEA; R IEMATODA; SECERNENTEA; R IEMATODA BANKS. MK/DDBJ DATA BANKS. MEMBRANE PROTEIN (POTE 19.9. TITAL. TITAL.	Score 454; DB 11; Length 341; Pred. No. 7.00e-67; 66; Mismatches 90; Indels 12; Gaps 11;
23 95 4.5 366 2 BRB2 24 96 4.5 397 7 PXX3- 25 96 4.5 615 6 NVPO- 26 96 4.5 615 6 NVPO- 28 95 4.5 727 10 VDA7- 29 93 4.4 274 1 BACH 30 94 4.4 518 1 XADC- 31 93 4.4 518 1 XADC- 32 92 4.3 113 5 INMO- 33 91 4.3 37 10 XADC- 34 94 4.4 1073 5 ITARC- 35 91 4.3 37 10 VZ48 36 91 4.3 518 1 XADC- 37 91 4.3 518 1 XADC- 38 91 4.3 518 1 XADC- 40 91 4.3 518 1 XADC- 40 91 4.3 518 1 XADC- 41 90 4.2 818 1 XADC- 42 90 4.3 113 5 INMO- 43 91 4.3 518 1 XADC- 44 90 4.2 561 10 VZ6N 45 90 4.2 561 10 VGLR- 44 90 4.2 561 10 VGLR- 45 90 4.2 561 10 VGLR- 45 90 4.2 561 10 VGLR- 46 90 4.2 561 10 VGLR- 47 NUSW- 45 90 4.2 561 10 VGLR- 47 NUSW- 48 90 4.2 561 10 VGLR- 48 90 VGLR- 48 90 VGLR- 48 90 VGLR- 48 NUSW- 48 NUSW-	RESULT 1	Query Match Best Local Similarity 32.8%; Matches 82; Conservative

ä

Gaps

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178 yiyyrgisvdiklslivlylpvgmislcyivyryiklyhvkt-tkshyiailrrssgffl 236
                                                                                                                                                                                                                   48 YPYHDSTAASTVILLVGVGLPVSSIILGETLSVYCNLLHSNSFISNNYIATIYKAIGTFL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 lpvsmgamsvalvslsga-pfmsgffskdlmielsmmdssvtygcyllellgl-iftsfy 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; MOLLUSCA; PELECYPODA (BIVALVIA); PTERIOMORPHIA;
MYTILOIDA; MYTILIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC.1.6.5.3) (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 92354892.
HOFFMANN R.J., BOORE J.L., BROWN W.M.;
HOFFMANN R.J., BOORE J.L., BROWN W.M.;
GENETICS 1311:397-412(1992).
-i- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
EMBL; M83762; G473465; -.
EMBL; M83765, G342472; -.
PIR; S28760; S28760.
PIR; S28743; S28743.
                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.0%; Score 106; DB 7; Length 522; Best Local Similarity 28.8%; Pred. No. 8.52e-02; Matches 23; Conservative 25; Mismatches 28; Indels
                                                                                                      Score 105; DB 8; Length 430;
Pred. No. 1.16e-01;
14; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROKARYOTA; FIRMICUTES; COCCI; STREPTOCOCCAEAE.
                                                               48627 MW; F942DF84 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 AA; 57217 MW; 97A15C3A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1994 (REL. 30, CREATED)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-0CT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                            522 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         719 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PENICILLIN-BINDING PROTEIN IA (PBP-1A).
PONA OR EXP2.
  POTENTIAL. POTENTIAL.
                                             POTENTIAL
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STRAIN-45607, AND 63915;
MEDLINE; 93010977.
MARTIN C., SIBOLD C., HAKENBECK R.;
EMBO J. 11:3831-3836(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 sari-vfsvmlgsn-yvnns 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYTILUS EDULIS (BLUE MUSSEL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 GETLSVYCNLLHSNSFISNN 94
                                                                                                        Query Match 5.0%;
Best Local Similarity 31.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREPTOCOCCUS PNEUMONIAE.
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  342
373
400
430 AA;
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Q04707;
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                                                                                                                                                                                                                                                                            237 £ 237
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TRANSMEM
TRANSMEM
TRANSMEM
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                                                                  SEQUENCE
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STRAIN-LT2;
MEDLINE; 91260454.
JIANG X.-M., NEAL B., SANTIAGO F., LEE S.J., ROMANA L.K., REEVES P.R.;
MCL. MICROBIOL. 5:695-713(1991).
-1- PATHWAY: O ANTIGEN SYMPHESIS IN LIPOPOLYSACCHARIDE BIOSYNTHESIS.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
PIR; 515308; 515308.
STYGENE; SG10453; RFBX.
LIPOPOLYSACCHARIDE BIOSYNTHESIS; TRANSMEMBRANE.
TRANSMEM
23 39 POTENTIAL.
TRANSMEM
45 61 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SALMONELLA TYPHIMURIUM.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 RVKEGRLSFYSGHSSFSMYCMLFVALYLQARMKGDWARL-LRPTLOFGLVAVSIYVGLSR 218
                                                                                                                                                                                                                                                                                                                     MITOCHONDRION.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 raieastkyfltgaaasal-llfssln-nawltgewsildltnplscatmtiaicmklg- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
                                                                                                                                                                                                                                                                                                                                                                          Score 121; DB 7; Length 345;
Pred. No. 6.87e-04;
27; Mismatches 28; Indels
                                                                                                                                                                                                          21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                 345 AA
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POTENTIAL.
                                                                                                                                                                                                                                                                                               XENOPUS LAEVIS (AFRICAN CLAWED FROG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 lapf-hfwlpevlqglslttgl1 129
                                                                                                                                                                                      21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEGO
01-NOV-1990 (REL. 16, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.3%;
Matches 21; Conservative
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                    273 wtdlfsnnst 282
                                             :|:| ::
247 VSDFFKERTS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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RFBX_SALTY
P26400;
01-x
                                                                                                                        RESULT 2

10 NUZA_XENLA
AC 21-JUL-1986
DT 21-JUL-1986
DT 01-NOV-1990
EN NDH-UBIQUIN
GN HEDLIN
GN BLA, MP
C 1- CATALTI
DR EMBL; MOO2T
C 1- CATALTI
DR EMBL; MOO2T
C 2- CATALTI
DR EMBL; MOO2T
C 3- CATALTI
DR C 3- CATALTI
DR C 4- CATALTI
DR C 5- CATALTI
DR C 5- CATALTI
C 5- CATALTI
C 5- CATALTI
C 6- CATALTI
C 7- CATALTI
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LT 8
YCB9_PSEDE
P29942;
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
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IRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| :||:| : :: | :: | :| | || || : : | :: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). BELONGS TO THE CARI/CYHR SUBFAMILY.

EMBL, M64932; G170849; -.
PIR; JC1173; JC1173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACYLATED BY PENICILLIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T -> A (IN STRAIN R6).

V -> I (IN STRAIN 63915).

E -> E (IN STRAIN R6).

E -> K (IN STRAIN 63915).

M -> I (IN STRAIN 63915).

E -> D (IN STRAINS 63915 AND R6).

S -> N (IN STRAINS 63915 AND R6).

S -> N (IN STRAIN 63915).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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Pred. No. 1.16e-01;
20; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SASNAUSKAS K., JOMANTIENE R., LEBEDIENE E., LEBEDYS J., JANUSKA A., JANULAITIS A., GENE 116:105-108(1992).
-!- FUNCTION: PROBABLE TRANSPORTER. CONFERS RESISTANCE TO CXCLOBEXIMIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X67873; G47420; -.
EMBL, X67872; G47418; -.
EMBL, 300527; G153768; -.
PIR: $28038; $28038.
PEPTIDOGLYCAN SYNTHESIS; ANTIBIOTIC RESISTANCE; CELL WALL;
                                                                                                                                                                                              STRAIN-R6X;
MEDLINE; 95020625.
PEARCE B.J., YIN Y.B., MASURE H.R.;
MOL. MICROBIOL. 9:1037-1050(1993).
-!- FUNCTION: CELL WALL FORWATION.
-!- THESE STRAINS ARE PENICILLIN'SENSITIVE.
-!- PATHANY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
-!- SUBCELLULAR LOCATION: EXTRACELULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANDIDA MALTOSA (YEAST).
EURARYOTA; FUNGI; DEUTEROMYCOTINA (IMPERFECT FUNGI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; JC1173; JC1173.
ANTIBIOTIC RESISTANCE; TRANSPORT: TRANSMEMBRANE.
TRANSMEM 100 120 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1993 (REL. 27, CREATED)
01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ^ A
                                                                                   XIIN C., BRIESE T., HAKENBECK R.;
BACTERIOL. 174:4517-4523(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYCLOHEXIMIDE RESISTANCE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79745 MW;
                                                                                                                                                                   SEQUENCE OF 293-369 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.0%;
Best Local Similarity 28.6%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MULTIFUNCTIONAL ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              657
719 AA;
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   [2]
SEQUENCE FROM N.A.
MEDLINE; 92325042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-VSB-889;
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                                                                                   MARTIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-972;
BADCOCK K. CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 GLPVS-SIILGETLSVYCNLLHSNSFISNNYIATIYKAIGTFLFGAAASQSLTDIAKY-S 123
                                                                                                                                                                                                                                                                                       450 ligmalfavgafiifqtlfnymavsfkveylasvfssnaffrsvsagafplfgralynnl 509
                                                                                                                                                                                                                                                                                                             62 LVGVGL-PVSSIILGETLSYYCNLHSNSFISNNYIA-TIYKAI--GTF-LFGAAASQSL 116
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
9
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-1- DOMAIN: COMPOSED OF THREE HONOLOGOUS DOMAINS.
-1- SIMILARITY: BELONORGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-1- SIMILARITY: BELSESTO?;
-1- SIMILARITY: MITOCHONDRION; INNER MEMBRANE; REPEAT;
HYPOTHETICAL PROTEIN; MITOCHONDRION; INNER MEMBRANE; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 345;
                                                                                                                                                                                                                  Length 552;
                                                                                                                                                                                                                Score 104; DB 3; Length 552 Pred. No. 1.57e-01; 29; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 mksrlsgsglglsdpqihmcsaslgeiaacivrvptevikq 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101; DB 11;
Pred. No. 3.86e-01;
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D059679A CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 AA
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POTENTIAL.
POTENTIAL.
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               POTENTIAL.
POTENTIAL
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83 103
28 148
0 240
282
316
339
38451 MW; L
                                                                                                                                                                                 61366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.7%;
Matches 29; Conservative
                                                                                                                                                                                                                    4.98;
                                                                                                                                                                                                                                  Best Local Similarity 25.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296
319
345 AA;
                                                                                                                                                                                                                                                                                                                                                                510 s-idkfpvgw 518
                                                                                                                                                                                                                                                                                                                                                                                                  117 TDIAKYSIGR 126
                                                                                                                                                             518
552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                    GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN
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Best Local Similarity 30.2%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                 C-TERMINAL OF M, E, AND NS1
                                                                                                                                                                                                                               VIROLOGY 162:167-180(1988).
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11174
22298
2302
2454
2482
                                                                                                                                                                                                                                                                                    STRAIN-NEW-GUINEA;
                                                                                                                                                                                                                                                                                                 MEDLINE; 89299482
WRIGHT P.J., CAUCH
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11174
22298
23302
24554
3388
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                                                                                                                        FLAVIVIRUSES.
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SITE
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                           102 vlkailpfiliaialyfglkpnmgdvdqh-srvtpfvftltlvp-ligfydgvfgpgtgs 159
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANTATORE P., ROBERTI M., RAINALDI G., GADALETA M.N., SACCONE C.; J. BIOL. CHEM. 264:10965-10975(1989).

-1. CATLATIT CATLATIT: NADH + UBIQUINONE - NAD(+) + UBIQUINOL. EMBL; JO4815; G453499; -. PIR; B34284; B34284.
                                                                                          GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                             CROUZET J. LEVY-SCHIL S., CAMERON B., CAUCHOIS L., RIGAULT S., ROUZET J., LEVY-SCHIL S., CAMERON B., THIBAUT D.;
J. BACTERIOL. 173.6074-6087(1991)
J. BACTERIOL. 173.6074-6087(1991)
EMBL. MGZGGG, GS51299;
PIR. 138164; 138164
HYPOTHETICAL PROTEIN; MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Mismatches 26; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                         ω
:
                                                                                                                                                                                                                                                                                                                                        Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION.
EURARYOTA, METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
EDECHINOIDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 352;
                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches 21; Indels
01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-UUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.4 KD PROTEIN IN COBO 3'REGION (ORF9).
PSEUDOMONAS DENITRIFICANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1989 (REL. 12, CREATED)
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                     Score 100; DB 11;
Pred. No. 5.19e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7; Lv
6.96e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION. SEQUENCE 352 AA; 39009 MW; 39BB4327 CRC32;
                                                                                                                                                                                                                                                                                                      261 AA; 27374 MW; 5D508436 CRC32;
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(REL. 12, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARACENTROTUS LIVIDUS (COMMON SEA URCHIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 RVSDYKHHW-SDVLTGL--IQGALVA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 -laac-hfwlpdvlgglpfiggliia 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        larity 32.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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es 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 89291831.
                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 92011366.
                                                                                                                 PSEUDOMONADACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1989
01-OCT-1989
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P12823;
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P12771;
                                                                                              PROKARYOTA:
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                                                                                                                                                                                                                                                                                                          SEQUENCE
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Matches
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         PROTEIN (ENVELOPE GLYCOPPOTEIN W): MAJOR ENVELOPE PROTEIN E;
NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3);
NAN-DIRECTED NA POLYMERASE (EC 2.7.7.48) (NS5)).
DENGUE VIRUS TYPE 2 (STRAIN PRISS)(S1).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
C (CORE PROTEIN); MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 88101365.
HAHN Y.S., GALLER R., HUNKAPILLER T., DALRYMPLE J.M., STRAUSS J.H.,
STRAUSS E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-DIRECTED RNA POLYMERASE (NS5).
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Pred. No. 5.19e-01;
20; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONSTRUCTURAL PROTEIN NSI.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
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DEAH BOX.
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Gaps

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Length 443;

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STRAIN-AKG31;
KERESZT A., SLASKA-KISS K., PUTNOKY P., BANFALVI Z., KONDOROSI A.;
SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: REQUIRED FOR THE BIGGENESIS OF C-TYPE CYTOCHROMES.
POSSIBLE SUBUNIT OF A HEME LYASE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHIZOBIUM MELLICTI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PLASMA MEMBRANE ATPASE 2 (EC 3.6.1.35) (PROTON PUMP) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i - SIMILARITY. BLONGS TO THE CCMF/CYCK/CCL1/NRFE/YCF5 FAMILY. BMBL; X82560; G575372; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOCHROME C-TYPE BIOGENESIS; TRANSMEMBRANE; INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 lylgyvgfsv-cfsfavaaliegridaawarwvrpwtlaawtfltagiamg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 676;
                                                                                                                                                                                                                   11; Indels
                         Q -> R (IN REF. 1).
T -> I (IN REF. 1).
R -> K (IN REF. 1).
T -> S (IN REF. 1).
G -> R (IN REF. 1).
G -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches 15;
                                                                                                                                                                            Score 97; DB 6; L
Pred. No. 1.24e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 98; DB 2; I Pred. No. 9.31e-01;
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C9947521 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK.
                                                                                                                                                                                                                      9; Mismatches
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                                                                                                                                                                                                                                                               280 pfysqnksfvkqicdlfislfalnkanagwlr 311
                                                                                                                                                                                                                                                                                      167 SFYSGHSSFSM-YCMLFVALYLQARMKGDWAR 197
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larity 34.4%;
Conservative
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Local Similarity 35.3%;
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                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                           88
215
379
397
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Best Local Similarity 3
           MOM
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617
676 AA;
                                                                                                                                443 AA;
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  SGD; L0001051; M
CONFLICT 88
CONFLICT 215
CONFLICT 379
CONFLICT 397
                                              215
379
397
412
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PMA2_LYCES
P23980;
01-NOV-1991 (
01-NOV-1991 (
01-FEB-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHIZOBIACEAE.
                                                                                                                                                                                                                                                                                                                                                                    CCMF_RHIME
CCMF_RHIME
P45404;
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TRANSMEM
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ID PM
AC P2
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DT 01
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1306 plfltssqqkadwipla-ltik-ginptaiflttlsrtsk-krswp-lneaimavgmvsi 1361
                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 iskshhpraieatikyfltqstasal-ilfssm-tnawstgqwditqlnhptscl-mltm 100
                       153 ICRGNAERVKEGRLSFYSGHSSFSMYCMLFVALYLQARMKGDW--ARLLRPTLQFGLVAV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 4.6%; Score 97; DB 6; Length 346; Best Local Similarity 26.0%; Pred. No. 1.24e+00; Matches 25; Conservative 33; Mismatches 28; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STAIN-SERGE / AB972;
STREITON J., CHURCHER C.M., BARRELL B., RAJANDREAM M.A., WALSH S.V.;
STREITON J., CHURCHER C.M., BARRELL B., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- FUNCTION: ESSENTIAL FOR MITOTIC GROWTH. MEDIATE ORGANELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                              | (1) | SEQUENCE FROM N.A. | SEQUENCE FROM N.A. | RA | SEQUENCE FROM N.A. | RA | SEQUENCE FROM N.A. | RA | DESJARDINGS P., MORAIS R.; | S. | MOL. BIOL. 212:599-634(1990). | CC -1- CARALYTIC ACTIVITY: NACH + UBIQUINONE = NAD(+) + UBIQUINOL. | DR | EMBL; X52392; G12962; -- DR | PIR; S10188; S10188. | S10188. | S10188. | S10188. | S10188. | ASIGNAL SIDERIAN | SEQUENCE | 346 AA; 38333 MW; 60A7C67B CRC32; | CONTROL SIDERIAN | CONTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHERITANCE.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SUBLELLULAR LOCATION: CYTOPLASMIC.
-1- SUBLARITY: LOW, TO VIMENTIN AND OTHER INTERMEDIATE FILAMENTS.
EMBL; X66371; G3916; -.
EMBL; Z49210; G798896; -.
PIR: A42636; A42636.
LISTA: SC00593; MDM1.
                                                                                                                                                                                                                                                                             01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDM1 OR YML104C OR YM8339.15C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA: FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 alaikiglvp-f-hfwfpeviggsslitallistim 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 SIYVGLSRVSDYKHHW-SDVLTG--LIQGALVAILV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
STRUCTURAL PROTEIN MDM1.
                                                                                                                                                                                                                 346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 AA
                                                                                                                                                                                                                 PRT;
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MEDLINE; 92332295.
MEDLINE; 92332295.
J. CELL BIOL. 118:385-395(1992).
                                                                                                                                                                                                                                                   01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEO)
01-NOV-1990 (REL. 16, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (REL. 27, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                GALLUS GALLUS (CHICKEN).
                                                                                  1362 las 1364
                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION
                                                                                                                            242 LVA 244
                                                                                                                                                                                                            NU2M_CHICK
P18937;
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Q01846;
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Gaps

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THE STATE OF THE S

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-1. CATALITIC ACTIVITY: APP + H(2)O = ADP + UNTHURHUGE HALL.
-1. SUBUNIT: POSSIBLY EXISTS AS AN HOMODIMER OR AN HOMOTRIMER.
-1. SUBCHLUARA LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1. AS MANY AS 6 TO 8 CLOSELY RELATED GENES MAY ENCODE OTHER ISOFORMS OF PLASMA MEMBRANE ATPASE IN TOWATO, LIKE THE LHAI GENE PRODUCT WHICH IS 96% IDEWTICAL TO THE LHAZ GENE PRODUCT.
-1. SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (EL-EZ-ATPASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACILLUS FIRMUS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 fwaayet-gffprvfgvstlgrtatddfrklasalylgvstisgallfvtrsrswsfver 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92332419.
IVEX D.M., GUFRANTA.A., SHEN Z., KUDYAN N., KRULWICH T.A.;
J. BACTERIOL. 174:4878-4884(1992).
-!- FUNCTION: THIS ELECTRONBUTRAL ANTIPORTER EJECTS ONE CD(2+) WHILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                             EWING N. WIMMERS L.E., MEYER D.J., CHETELAT R.T., BENNETT A.B.; PLANT PHYSIOL. 94.1874-1881(1990).
-!- FUNCTION: THE PLASMA MEMBRANE ATPASE OF PLANTS AND FUNGI IS A HYDROGEN ION POMP. THE PROTON GRADIENT IT GENERATES DELVES THE ACTIVE TRANSPORT OF NUTRIENTS BY B+- SYMPORT. THE RESULTING EXTERNAL ACIDIEICACTION AND/OR INTERNAL ALBINIZATION MAY MEDIATE GROWTH RESPONSES.
                                                                                                                                                                                                                                                                                                              PROSITE: PS00154; ATPASE E1_E2.
HYDROLASE; HYDROGEN ION TRANSPORT; TRANSMEMBRANE; PHOSPHORYLATION;
ATP-BINDING; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1.-) (CADMIUM EFFLUX
            LYCOPERSICON ESCULENTUM (TOMATO).
EUKARYOTR: PLANTA: EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
SOLANALES; SOLANDAEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
ATP (BY SIMILARITY).
CICH2D8A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98; DB 7; Length 704;
Pred. No. 9.31e-01;
19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                    3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRACELL.
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               723 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
8 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        539 pglllvvalivaqlvatliavyas 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 WSDVLT-GLIQGALVAILVAVYVS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - APR-1993 (REL. 25, CREATED)
- APR-1993 (REL. 25, LAST SEC)
- OCT-1994 (REL. 30, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 27.4%;
Matches 23; Conservative
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5563
578
704
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444
460
484
                                                                    SEQUENCE FROM N.A.
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P30336;
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DOMAIN
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Search completed: Tue Nov 4 10:21:36 1997 Job time: 55 secs.

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                                                                                                                                                                                                                                                                                                                                                                                                                        159 ERVKEGRLSFFSGHSSFSMYCMLFVAL-YLQARMKGDWARLLRPTLQFGLVAVSIYVGLS 217
ACCUMULATING TWO PROTONS BY AN ENERGY-DEPENDENT EFFLUX MECHANISM
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                              11- SIMILARITY: CONTAINS A COPY OF THE HEAVY-METAL-ASSOCIATED (HMA)
                                                                                                                                                                                                                                                                                                                                                           9
             -:- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS POTENTIAL TRANSMEMBRANE DOMAINS.
-:- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                                                                                                                         Length 723;
                                                                                                                                                                                                                                                                                                                                                         18; Mismatches 16; Indels
                                                                                                                                                                                                                                           CADMIUM (POTENTIAL).
CADMIUM (POTENTIAL).
PHOSPHORYLATION (PROBABLE).
65222CA5 CRC32;
                                                                                                                                                                                            HYDROLASE; TRANSMEMBRANE; PHOSPHORYLATION; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                         Score 97; DB 2; I
Pred, No. 1.24e+00;
                                                                                                                                                                                                             CADMIUM RESISTANCE; METAL-BINDING
                                                                                                                                        PIR; D42707; D42707.
PROSITE; PS00154; ATPASE_E1_E2.
PROSITE; PS01047; HMA.
                                                                                                                                                                                                                                                                                        78207 MW:
                                                                                                                                                                                                                                                                                                                      y march 4.6%;
Local Similarity 33.3%;
nes 20; Conservative
                                                                                                                             EMBL; M90750; G143753; -.
                                                                                                                                                                                                                                                                         412
723 AA;
                                                                                (E1-E2 ATPASES)
                                                                                                                                                                                                                                           METAL
METAL
MOD_RES
SEQUENCE
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Thu Nov 6 11:57:37 1997; MasPar time 148.35 Seconds 958.178 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-842-827-5 (1-1362) from US08842827.seq 1362 Title:

.....AAAATTTTTTTTTTTTTT Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 .. STD Nmatch

142080 seqs, 52183452 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-geneseq28 Database:

1.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part11 18:part18 19:part18 24:part20 21:part21 22:part22 23:part23 24:part29 25:part25 26:part26 27:part27 28:part28

Mean 9.460; Variance 6.196; scale 1.527 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•					
Result		Query					
چ	Score	Match	Match Length DB	8	Ω	Description	Pred. No.
ч	81	5.9	1047	7	010572	Human Natriuretic Pep	4.20e-31
~	67	4.9	1047	N	010572	Human Natriuretic Pep	6.44e-23
m	48	3.5	91	ø	051746	Oligonucleotide probe	3.06e-12
4	45	3.3	91	σ	051746	Oligonucleotide probe	1.27e-10
'n	ტ წ	2.0	204	Н	N81164	Base substituted E.co	1.83e-07
φ	39	2.9	204	Н	N81164	Base substituted E.co	1.83e-07
7	38	2.8	114	12	970467	Generic DNA sequence	6.00e-07
æ	36	5.6	114	12	070467	Generic DNA sequence	6.24e-06
σ	36	5.6	114	12	070468	Generic DNA sequence	6.24e-06
10	36	5.6	114	12	270466	Generic DNA sequence	6.24e-06
Ξ	36	2.6	114	12	070465	Generic DNA sequence	6.24e-06
12	32	5.6	114	12	070469	Generic DNA sequence	1.99e-05
13	36	5.6	114	12	070468		6.24e-06
14	35	2.6	114	12	070469	Generic DNA sequence	1.99e-05
12	34	2.5	114	12	970470	Generic DNA sequence	6.25e-05

10-JAN-1991

	-	1.82e-03	•	5.98e-04	5.45e-03	7.	1.61e-02	1.61e-02	1.61e-02		1.35e-01		1.35e-01	•		3.80e-01		•	3.80e-01	3.80e-01	1.05e+00	1.05e+00	2.85e+00	•	•	ω.	2.85e+00	2.85e+00	1.05e+00
DNA	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	HSV-1 gB and surround	Generic DNA sequence	Generic DNA sequence	Primer used in the la	Generic DNA sequence	DNA	Generic DNA sequence	DC43 TSAR library gen	DC43 TSAR library gen		Ballast Constituent c	Mixed oligonucleotide	-	TSAR library	TSAR library	HCV envelope region n	HSV-1 qB and surround	Mixed oligonucleotide	DC43 TSAR library gen	Streptomyces protease	Sequence encoding new	Sequence encoding new		Sequence encoding new	ast sp	Endoglucanase (58 kDa
070465	070466	970472	070470	N71302	070471	270471	T14322	070473	070473	970472	T13611	T13610	035072	011195	051787	T13613	T13612	T13610	035072	N71302	051787	T13612	N70195	N50034	N50024	N50032	N50030	T51183	T29032
77	12	12	12	7	12	12	7	12	12	12	21	21	ø	7	7	21	7	21	9	~	۲	21	7	m	٣	3	m	28	23
114	114	114	114	3871	114	114	67	114	114	114	81	85	565	36	a	74	75			3871		75	201	498	501	501	501	787	1511
	٠	٠	٠	2.3	•	•	•	2.1	2.1	٠	٠	•		•	1.9	1.9	1.9	1.9	1.9	1.9	1.8	1.8	٠		1.8	1.8	1.8	1.8	1.8
34	34	31	31	32	30	30	29	29	58	28	27	27	27	26	36	56	26	26	26	26	25	25	24	24	24	24	24	24	25
16	17	8	19	70	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	43	43	44	45
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ALIGNMENTS

09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; ENP; CNP; kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
Homo sapiens. Domain 23..455
/label-extracellular domain
/note= "binds natriuretic peptides A,B and C]"
Domain 456..456
/label- transmembrane domain 479..1047 /label = cytoplasmic domain /hote= "GC and protien kinase activity" Modified -site 24..26 Location/Qualifiers J. 1 Q10572 standard; DNA; 1047 BP. Q10572; /label= N-glycos_site
Modified -site 35.37
/label= N-glycos_site
Modified -site 161.163
/label= N-glycos_site
Modified -site 195.197 Modified -site 277..279
/label= N-glycos_site
Modified -site 349..351
/label= N-glycos_site
Modified -site 600..602 /label- N-glycos_site Modified -site 244..246 /label- N-glycos_site Modified -site 277..279 /label= signal sequence /label= N-glycos_site WO9100292-A. Protein 12 /label = mature NPBR Peptide RESULT DACKER COLORS OF THE COLORS OF

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RESULT
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                                                       Chang M, Goeddel D, Lowe D;

N PFSDB, 010324.

N PFSDB, 010324.

N PFSDB, 010324.

N RITHLETL protein receptor B - for diagnosis and treatment of the sequence was derived from the DNA encoding natriluretic peptide.

The sequence was derived from the DNA encoding natriluretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein the become sequence was derived from the DNA encoding natriluretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein the protein.

The sequence was derived from the DNA encoding natriluretic peptide of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-NPRB analogues). The protein (or variants) can be used in treatment of natriluretic peptide disorders, and also to isolate peptides using confinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1062 GAACATCACTGGGATGGTGCTTGTGGTCATACGCGAGACAGTCCCGTGTAGAAGGCCA 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 nnsavdnknyhdndnnngngcvynaasvarnashwrnnnntagavasgnsakndhyrtnv 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nvyaronggnnnathnnrangrnvyncgnnnmnhnnnnnnntnngdyvnnyndvngn 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrryhgvtgnv 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vmdknndrntdnvnwamgdndsg-dnnnaahysganknnwwtgrnnnwvkgannsdnnnc 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 ACAGCCAAAGAGGAAGCAGCCCACTTGCTTATAGAGTGCTGCCACGTAGGGGTTCTGAAT 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 andnddnscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmnwrnrwnnn 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rysnandavkgmannhasnasshgsakssacvvdsravakatdygnasarstanaddana 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 vrngnrnynrnsndrtnnnnnnnnnnrcwandnanrndngnnkgnnrrnnknggtsnnd 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1002 T-CATGATCAAGGTGAACTGCAGGAGGGGCCCGGAGCAGGCGGGCTCCTCGCCAAGTGAAG 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         garnntnavvnnnhnnsyawawnrvgnavanavnangrannvdnrnvssnnngacsnyna 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 rtgnsankngnnvvtnhghnnwtaraannyndartddrnhyntnngvnnanngsnnsvnh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 CGTCGA-CCGCGACTTCTTCAGGTAATAGATCCGGTAGAATTCCCCCGTGATGATCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAATGTAGCCTTCAGAGCAGTTGATCTGGCTGAAATCAGGGTTGCAGACACTCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGATGAGCAGCACCGGCTTGCT - GCCGCTCCTCGGGTTGTTGTTGAGCGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 883 GAGAAGAAGGACTICCIGGCIICCIGGACTIIGCIGICAICACCICTGCATCIGIAGIIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                763 TGAGGACGCAGGCGCCCTATGGACACTTTGGCAATGT-CTGTGAAAGACTGGCTGATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                      Match 5.9%; Score 81; DB 2; Length 1047; Local Similarity 8.7%; Pred. No. 4.20e-31; es 83; Conservative 265; Mismatches 598; Indels
                                                                                                                                                                                                                                                                                                                                                                                51 T;
                                                                                                                                                                                                                                                                                                                                                                                83 G;
                                                                                                                                                                                                                                                                                                                                                                              15 C;
                                                                                                                                                                                                                                                                                                                                                                                87 A;
22-JUN-1990; U03586.
23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                            1047 BP;
                                                                                                                                                                                                                                                                                                                                                      also be prepd
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349 CIGCCGCCGTTCTTGCTCTCCGGGACGATCGCTTTGTCGTACTTGTAGTTTTGCGCG 290
                                                 onnormonyannonkovoortnayonnkrkanannyonnohsvannokrgotvoanands 859
                                                                                                               vtnynsdnvgntansans-tnmnvvtnnndnytcndanndnndvykvntngdaymvvsgn 918
                                                                                                                                           229 AGGCGCCCGGGTCGCCTCCTGGCCGAGGCTGCGGATAGTGGCGGGTCGGCCCCGGCT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natification protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc.

Claim 3; Fig 1; 4Pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein finase activity. The DNA can be inserted into expression vectors for the prodon. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952).

The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using also be prepd.
                                                                                                                                                                                                                                                                                                           09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                               919 ngrngnrhannnarmananndavssnrnrhrnhdnnrnrngvhtgnvcagvvgnk 973
                                                                                                                                                                                                    169 CCGGGCGCGCGCTAGAGTGCAGCCGGGGCTGCCTGCTAGCTGCAAAAGGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
/label- extracellular domain
/note- "binds natriuretic peptides A,B and C]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "GC and protlen kinase activity"
Modified -site 24..26
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                            Q10572 standard; DNA; 1047 BP Q10572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain 456..456
/label= transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= cytoplasmic domain
/note= "GC and protien kina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- N-glycos_site
Modified -site 349..351
/label- N-glycos_site
Modified -site 600..602
/label- N-glycos_site
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Modified -site 244.....
/label- N-glycos_site
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Modified -site 35, 37
/label- N-glycos_site
Modified -site 161.163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..197
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/label- signal sequence
Protein 12
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Modified -site 195..1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             label - mature NPBR
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287 GOTTGCGGCGCGAGCCTCCCGCCCGCGAAGACGTCCCGCAACAGCAGCACCACACACCC 230
                                                                                                                                                                                                                                                                                                                                        1 ggctccggcgssvhsyyvvhvvshhhsvhhvvhhvsvvvvhhvvhvvhhvhyhvyv 58
                                                                                                                                                               claim 3; Page 14; 23pp; English.
Oligonucleotide probe MX14 consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 057735-45 and 051747-59.
Sequence 91 Bp. 77, 75, 17, 15 G; 4 T;
                                                                                                                           New oligo:nucleotide probes specific for Mycobacteria – used detection and amplification of Mycobacteria nucleic acid in
                                                                                  (BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                3.5%;
Best Local Similarity 15.5%;
Matches 9; Conservative
                                                       24-MAY-1993; 108325.
26-MAY-1992; US-889651
                                                                                                  Spears PA;
                                                                                                            WPI; 93-378844/48.
New oligo:nucleotide
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                              EP-571911-A
                                           01-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                Synthetic
                                                                                                  Shank DD,
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                                                                                 grannvdnrnvssnnngacsnynannsavdnknyhdndnnngngcvyna-asvarnashw 115
                                                                                                         GGACITIAGAACGATITAGGGIT-GACAGAGGAAAGCAGAGGCGCGCGCAGGAGGAGCAGAA 108
                                                                                                                                       rnnnntagavasgnsakndhyrtnvrtgnsankngnnvvtnhghnnwtaraannyndart 175
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                                                                                                                                                                                                                                                     nnnnnanrnnntngdyvnnyndvngnsnragntratgrnwndnrtrnnananrnanntvn 294
                                                         Gaps
                                                                                                                                                        ddrnhyntnngvnnanngsnns-vnhnvyarnnggnnnathnnrangrnvyncgnnnmnh
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                                                                                                                                                                                                                                                                             vatyrnnnnnnynnnnrnnnrarndngvnngnsnmnnagcnydgnnnyanvnnntnnn
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                                                       13;
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051746;
31-MAY-1994 (first entry)
0119onucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                            DB 2; Length 1047;
                        Ouery Match
4.9%; Score 67; DB 2; Length 1047;
Best Local Similarity 8.7%; Pred. No. 6,44e-23;
Matches 75; Conservative 246; Mismatches 532; Indels
   51 T;
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 83
 15 C;
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87
BP;
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 Sequence
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Gaps

5; Indels Length 91;

Pred. No. 3.06e-12; Score 48; DB 9; 44; Mismatches

MK14 but

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but
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N81164, Standard; DNA; 204 BP.
N81164, Standard; DNA; 204 BP.
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                 nseq
                                                                       31-MAY-1994 (first entry)
Oligonuclectide probe MK14-A
Oligonuclectide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                           New oligo:nucleotide probes specific for Mycobacteria – user detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 9; Length 91;
Pred. No. 1.27e-10;
45; Mismatches 7; Indels
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                          BP
                                                                                                                                                                                                                                                                                                                          (BECT ) BECTON DICKINSON CO
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Best Local Similarity 11.9%;
Matches 7; Conservative
r 4
Q51746 standard; cDNA; 91
                                                                                                                                                                                                                                                              24-MAY-1993; 108325.
26-MAY-1992; US-889651
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misc_feature
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                                                                                                                                                                                                                                                                                                                  Disclosure; prizerous completened on molecules and screening.

Random point mutations were introduced into the alpha fragment of E-coll beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonuclectide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 and generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 ttthhyrrmrbnvyrdynrsdaawyccyrrsvkydccynachhddhyvybbbvynvhnh 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      929 ATACCIGCAGGCCCGCTICACITGGCGAGGAGCCCGCCTGCTCCGGCCC-CTC-CTGCAG 986
                                                                                                                                                                                                                                                        Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
Disclosure; p; English.
Estandom point mutations were introduced into the alpha fragment of
E.coli beta-qalactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 ayrccbgcaggycgacbcyrraggnyccccggggywccgagcycgaayycdchygccgymr 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N81164 standard; DNA; 204 BP.
N81164;
OB-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T; WPI; 88-279927/40.
                                                                                                                                                                                                                Lebtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 2.9%; Score 39; DB 1; Lv Local Similarity 18.1%; Pred. No. 1.83e-07; es 29; Conservative 68; Mismatches 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 C;
                      /function=multiple cloning site primer_bind 187..204
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                                                                                                                                                                                       (SUSO) SUOMEN SOKERI OY
                                                                                                                05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
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03-APR-1987; US-034819.
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Tidentifying proteins or peptide(s) which bind a ligand - by recening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain.

Tomprising a binding domain and an effector domain.

Disclosure: Page 35; 255pp; English.

O70467 is a generic DNA sequence used to generate random TSAR (Totally synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16/TGC) (NNB)16/NNB)16/TGC) (NNB)12. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in R5151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with septide peptide sext two functional regions - a binding domain with a fightity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oliqonicalcides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs confer some degree of conformational rigidity to the peptides. The TSARs confers one degree of conformational rigidity, eg. metal ion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 yrraggnyccccggggywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrdyn 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 rsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccbnnhvchnvhb 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 TGACGATCCCCACGGCACAGAGCACAGGGTCATTTATTGTCTCACCAGTTTTCAGTGGGT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generic DNA sequence to generate a random TSAR petide library. TSAR, totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
it to generate a popn of DNA molecules which terminate at all possible nuclectide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nuclectides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a sultable host-vector system. The sequence covers all 176 difft base substitutions, most of which see also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 204; Pred. No. 1.83e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      11 T;
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                                                                                                                                                                                                                                                                                                                                                                                                      47 C; 17 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 TCGATGAGGAAGGGGAGGCCCGCCAT 429
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55..60
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FOWLKES DM, RAY BK;
WPI; 94-279739/34.
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Best Local Similarity 16.8%;
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US-176500.
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Friends Roberts Formula and an effector domain by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English effector domain and an effector an also be compensated as follows: X(NUB) [CTCC] (NUB) [
                                                    the need for
radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromicentes, est monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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                                                                                                                                                                                                                                                                                                                                             404 GATGAGCACCCGCTTGCTGCCGCTCCTCCGGGTTGTTGTTGAGCGCCGGGCTGCC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generic DNA sequence to generate a random TSAR petide library.

SAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                            344 GCCGTTCTTGCTCTCCGGGACGATCGCTTTGTCGTACTTGTAGTTTTGCATG 293
                                                                                                                                                                                                    Length 114;
                                                                                                                                                                                               Score 38; DB 12; Length 114 Pred. No. 6.00e-07; 34; Mismatches 73; Indels
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55..60
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31-JAN-1994; US-189331.
(UYNC-) UNIY NORTH CAROLINA.
FOWLKSS DM, KAY BK;
WPI: 94-279739/34.
P-PSDB; R65153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             070467 standard; DNA; 114 BP.
                                                                                                                                                                                                  2.88;
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                                                                                                                                                                                                                                                    5; Conservative
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Best Local Similarity
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PT Trible Robinson or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; page 35; 255pp; English experses this generic formula can also be comprehence as fallinity Rangents! Deptides: This generic formula can also be comprehence as follows: X(NNB)lf(TGC)(NNB)52(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specific peptides generated by these generic sequences are shown in 070466-68. Comprehence are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with a fifthity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker operative between the 2 domains. The oligonuclectides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues positioned in, or flanking, the unpredicted or variant residues positioned in, or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, redisotope, peptide, toxin or enzyme, to the specific target or on the conclosal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody monoclonal or polyclonal antibodies and enced and have designed activity sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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                                                                                                               Generic DNA sequence to generate a random TSAR petide library. YSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatemented heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                          398 GCTCATCTGCCTCGACCTCTTCTGCCTCTTCATGGCGGGCCTCCCCTTCCTC 449
                                                                                                                                                       Length 114;
Length 114;
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Pred. No. 6.24e-06;
34; Mismatches 74; Indels
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  Score 36; DB 12; I
Pred. No. 6.24e-06;
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                                     34: Mismatches
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Q70468 standard; DNA; 114 BP
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(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Ray BK;
WPI: 94-279739/34.
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3.6%;
  3.68;
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                                       4; Conservative
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standard; DNA; 114 BP.
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WPI; 94-279739/34.
P-PSDB; R65150 and R65151.
                                                                                 (first entry)
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50,04666 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows:X(NNB)1(GC)(NNB)10(TGC)Z(NNB)4Z(NNB)6 (TGC)(NNB) (TGC)Z(NNB)10(TGC)Z(NNB)4Z(NNB) (TGC)(NNB) (TGC)Z(NNB)10(TGC)Z(NNB)4Z(NNB) (TGC)Z(NNB) (TGC
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                                                                                                                                                                                                                                                                                           Generic DNA sequence to generate a random TSAR-9 petide library. TASR: totrally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid: detection; screening; treatment; generic; ss.
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                                                                                                      386 CAAGGGGGTGCTGCTCATCTGCCTCGACCTCTTCTGCCTCTTCATGGCGGGC 437
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31; Mismatches 71; Indels
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Q70466 standard; DNA; 114 BP.
Q70466;
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(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
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US-176500.
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94-279739/34.
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Condition a generic DNA sequence used to generate random TSAR (Totally Statestor Affailty Reagents) peptides. This generic formula can also be represented as follows: X(NNB) G(TGC) (NNB) 14 (TGC) (TGC) (NNB) 14 (TGC) 
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Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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07047-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
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Pred. No. 6.24e-06;
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31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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PT Gentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or pertifying proteins and an effector domain

By Screening a recombinant vector library expressing fusion proteins

By Screening a binding domain and an effector domain

By Screening a binding domain and an effector domain

By Staclosure; Page 35; 255pp; English: This generic formula can also be

Cy0468 is a generic DNA sequence used to generate random TSAR (Totally

Cy0468 is a generic DNA sequence used to generate random TSAR (Totally

Cy0468 is a generic DNA sequence used to generate random TSAR (Totally

Cy0468 is a generic DNA sequence used to generate an also as a binding to an also be

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TSAR; tocally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatencated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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WPI; 94-279739/34.
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WO9418318-A.
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This generic formula can be represented as follows: X(TGC)(NNB)10-

Sites (X is not the same as Y) that are not specified further. This site is not the same as Y) that are not specified further. This can establish are cloverled in structure. Other sequences are shown in R61810-54. Takks are concatenated by these generic sequences are shown in R61810-54. Takks are concatenated heterofunctional proteins or peptides. Comparising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide continuals 2 or 4 dysteine residues positioned in, or flanking, the upredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or in conformation of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma conformation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid
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Generic DNA sequence to generate a random TSAR petide library.
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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Pred. No. 1.99e-05;
32; Mismatches 70; Indels
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                                                                                                                                sequence represents 'Z'; '
                                                      Location/Qualifiers
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Sequence 114 BP; 0 A; 4 C;
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                                                                                                                                                                                                                                                                                    01-FEB-1993; US-013416.
31-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
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Local Similarity 4.7%;
nes 5; Conservative
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Gaps

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Synthetic Affinity Reagents) peptides. This generic formula can also be

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Screening a recombinant vector library expressing fusion proteins

Comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

Of0466 is a generic DNA sequence used to generate random TSAR peptide

This generic formula can be represented as follows: X(TCC)(NNB)10-

This generic formula can be represented as follows: X(TCC)(NNB)10-

(TGC)(NNB)6Z(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction

sites (X is not the same as Y) that are not specified further. This

sequences are shown in Q70465-68. Other specific peptides

generated by these generic sequences are shown in R6150-54. TSARs are

concatenated heterofunctional proteins or peptides, comprising at least

two functional regions - a binding domain with affinity for a ligand and

a second effector peptide portion that is chemically or biologically

active. They may further comprise a linker peptide between the 2 domains.

The oligonucleotides are also designed so that the expressed peptide

conformational rigidity to the peptides. The TSARs or compsis.

TSAR binding domain can be used in vivo to deliver a chemically or

or enzyme, to the specific target or on the cell. They can also replace

the function of macromolecules, eg. monoclonal or polyclonal antibodies

conformation or in vivo antibody production. The TSARs are easily

charecterised and have designed activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generic DNA sequence to generate a random TSAR peptide library.
TSAR: totally synthetic affinity reagent: synthetic; binding domain;
effector domain; concetenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins
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Pred. No. 1.99e.05;
32; Mismatches 70; Indels
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Q70470 standard; DNA; 114 BP.
Q70470;
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Fowlkes DM, Ray BK;
WPI; 94-279739/34.
   UNIV NORTH CAROLINA.
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01-FEB-1993; US-013416.
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                                                                                                                                                                                                                                                                                            Edinburgh, U.K.
Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh,
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179:EST179
184:EST184
189:EST189
194:EST194
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176:EST176 1
181:EST181 1
186:EST186 1
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196:EST196 1
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ALIGNMENTS

1.63e-298 6.13e-295 2.29e-291 5.56e-270

ye74a10.rl Homo saple 0 MDB0538R Mouse brain, Human placenta cDNA 5 MDB0538 Mouse brain, Human placenta CDNA 5 yg25b02.rl Homo sapie

30 R71020 10 T92854 10 H77957 38 AA048371 0 H12562 13 W00564 17 W00564 177856 771976 5 AA135784 5 AA092191 W61641 HFC3 W6164 1 HFC3 W6164 1 HFC3 W6164 1 HFC3 W6164

yg25b02.rl Homo saple 1.10e-218
H. sapiens partial cD 3.76e-208
yc96f03.rl Homo saple 5.69e-182
and2b06.rl Stratagene 5.68e-173
zo54f04.rl Stratagene 6.24e-139

R19424 HSC3MH031 T78825 AA105463 AA156375

C18274 R75376 C16881 R75377 R00690

145 145 145 165 109

17-SEP-1996 sapiens cDNA clone EST Homo 8 pregnant uterus NbHPU to WP:T28D9.3 CE02068 mRNA ďď 555 b 1 Soares p similar t AA056693 zkBlb05.sl S 489201 3' si AA056693 g1549094 EST. LOCUS DEFINITION ACCESSION NID KEYWORDS

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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
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Eukaryotes, intochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 572)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                 Indels 10;
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Pred. No. 0.00e+00;
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/lab_host="DH10B"
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Washbr-Werck EST Project
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Washbr-Merck EST Project
Washbragton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Petrebratei, Eutheria; Primates; Catarrhini; Hominidae; Homo. [ kases 1 to 555]
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollann,M., Kucabb,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rhitin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Pred. No. 0.00e+00;
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/lab_host="DH10B"
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The WashU-Merck EST Project
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Best Local Similarity 98.9%;
Matches 548; Conservative
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                            Homo sapiens
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/sex.female"
/dev.stage-"adult"
/lab_host-"bH10B"
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21111f05.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone
501633 3',
AA135741
91696753
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: +40M13 fwd. from Amersham
High quality sequence stop: 393.
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollann,M., Rucaba,T., Le,M., Lemfon,G., Marra,M., Parsons,J., Riftin,L., Rohlfing,T., Soares,M., Ten,F., Marteston,R., Williamson,A., Wohldmann,P. and
       cggtcgacgattcagaacccctacgtggcagcactctataagcaagtgggctgcttcctc
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Washor-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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The WashU-Merck EST Project
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/note-forgan: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I oligo(dT) primer [5' and cDNA was primed with a Not I oligo(dT) primer [5' and cDNA was primed with a Not I and clouble-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Patima Bonaldo." /clone="50.613" /clone="50.613"
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Pred. No. 0.00e+00;
0; Mismatches 2;
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/organism="Homo sapiens"
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Db 301 tggtgcttgtggtctgatacgcgagacagtcccgtgtataaggccatcatggtcaaggtg 360 1048 1011	RESULT 5 LOCUS LOCUS LOCUS LOCUS LOCUS PERMITTON POBBILLS1 Homo sapiens cDNA clone 186812 3'. REST ACCESSION H50533 NID REYNORDS BST. SOURCE AND FAIR NOT I SELECT REACLACE CONDA WAS DIGATED TO I SOURCE CONDA SOURCE SOURC	TITLE Trevaskip.E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. JOURNAL Unpublished (1995) COMMENT Context: Wilson RK Washb-Merck EST Project CONTEXT: Washb-Merck EST Project Washb-Merck EST
SOURCE human. ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata Eutheria; Primates; Catarrhin; Hominidae; Homo. REFERENCE (bases 1 to 449) AUTHORS Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. TITLE The WashG-Werck EST Project JOURNAL Unpublished (1995)	CORMENT CONTACT: Wilson RK WashU-Merck EST Project WashIngton University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 316	Same retus as the retal lung library, Soares retal lung NDHL19M." Clone="11b-"Scares" Fetal Lung library, Soares retal lung NDHL19M." Clone="11b-"Scares" Fetal heart NDHH19W." Clone="11b-"Scares" Fetal heart NDHH19W." Gev_stage="19 weeks" Gev_stage="19 weeks

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US-08-842-827-5.rst

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/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                                                                         1 tttccctacattctactgtctgatgagattggagagcagcaagaacttgctgtcagcagt 60
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               Length 480;
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Score 402; DB 54; Le
Pred. No. 0.00e+00;
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               29.5%;
97.7%;
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Sarcopterygii; Choanata; Tetrapoda; Aminiota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
Hillar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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              301 cgcgagacagtcccgtgtagaaggccatcatgatcaaggtgaactncaggagggccgga
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO |
Fax: 314 286 1800
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/clone="152054"
107 c 133 q 113
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High quality sequence stops: 270
Source: IMAGE Consortium, LLNL
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                         Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                       /organism="Homo sapiens"
/clone="297839"
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                                                                                                                           Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
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                                Contact: Wilson RK
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            insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGGAG 3' -3' adaptor sequence: 5' CTCGAGTTPTTTTTTTTTTTTTT 3'"
/clone="SOT19"
/clone="Stratagene pancreas (#937208)"
/clone="Stratagene pancreas (#937208)"
/clone="Stratagene pancreas (#937208)"
/lab.host="Stratagene pancreas (#937208)"
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, C., Marra, M.
Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                        1 aamatcagtcgggcaaaagtttttccctacattctactgtctgatgagattggagagag
                                                                                                                                                                                                                                                                                                                                                                     atagcaggggcaggcagggagagcgtctttagtcttgaagaggtcagacacgaagaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    actatgcagcaggccaggggctccttgagcaaatcctgccagaacatcactgggatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1045 IGCTIGIGGIC-TGATACGCGAGACAGICCCGIGTAGAAGGCCATCAIGAICAAGGIGAA
                                                                                                                                                                                                            ë,
                                                                                                                                                                           Length 428;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 bp mRNA EST
Homo sapiens cDNA clone 297839 3'
                                                                                                                                                                           Score 401; DB 191;
Pred. No. 0.00e+00;
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson, R.
The WashU-Merck EST Project
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                                                                                                                                                                           29.4%;
98.8%;
                                                                                                                                                                                                         419; Conservative
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 419: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p1713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ostelchthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1165 ATAGCAGGGCAGGCAGGGAGAGCGTCGTCTTAGTCTTGAAGAGGTCAGACACGAAAAA 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1105 ACTATGCAGCAGCCACCA-GGGCTCCTTGAGCAAATCCTGCCAGAACATCACTGGGATG 1047
                                                                                                                                                        1345 AAAATCAGTCGGGCAAAAGTTTTTCCCTACATTCTACTGTCTGATGAGATTGGAGAGCAG 1286
                                                                                                                                                                                                                                                         1285 CAAGAACTIGCIGICAGCAGICATITIACAAAACAGCICAGGAGGIGGGIGGCACCIAC 1226
                                                                                                                                                                                                                                                                                                                                                            181 atagcaggggcagggcagggagagcgtcgtcttagtcttgaagaggtcagacacgaagaaa 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 actatgcagcagcaccacgggctccttgagcaaatcctgccagaacatcactggatg 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1046 GTGCTTGTGGTCTGATACGCGAGACAGTCCCGTGTAGAAGGCCATCATG-ATCAAGGT-G 989
                                                                                                   1 aaaatcagtogggcaaagtttttccctacattctactgtctgatgagattggagagag 60
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     Length 413;
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                                                 ö
Score 388; DB 102;
Pred. No. 0.00e+00;
0; Mismatches 0;
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RESULT

KEYWORDS

SOURCE

REFERENCE AUTHORS

TITLE

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Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata, Eukaryotae, Metazoa, Eumetazoa, Bilateria, Goathostomata, Osteichthyes, Deuterostomia, Choanata, Vertebrata, Gnathostomata, Osteichthyes, Saroopterygii, Choanata, Terrapoda, Anniota, Mammalla, Theria, Eutheria, Archonta, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 446)
Hillier, L., Clark, M., Dubuque, T., Eliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lenon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stops: 153
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1034 AGACCACAAGCACCAT-CCCAGTGATGTTCTGG-CAGGATTTGCTCAAGG-AGCCCTGGT 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agaccacaagcaccattcccagtgatgttctgggcaggatttgttcaagggagccngggt 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676 AGCAAGTGGGCTGCTTTCCTTTTGGCTGTGCCATCAGCCAGTCTTTCACAGACATTGCCA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 aagtgtccatagggcgcctgcgtcctcacttcttgagtgtctgcaaccctgatttcagcc 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agcaagtgggctgcttcctctttggctgtgcctcaagccagtctttcacagacattgcca
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                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
WashUn-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 17; Indels
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Pred. No. 0.00e+00;
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        - oligo(dT) primer [5'
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122 c 1
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1 Similarity 94.8%;
423; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
High quality sequence stops: 97
Source: IMAGE Consortium, LUN.
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 tacatcatgttgtggtgattgttcctgtcaataatntccacaggtgaaggatttccttc 180
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Butheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,M., Parsons,J., Rikhu,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048 TGGTGCTTGT-GGTCTGATACGCGAGACAGTCCCGTGTAGAAGGCCATCATGATCAAGGT
                                                                                                                                                                                                                          Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fat: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 402;
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Y115h04.rl Homo sapiens CDNA clone 139351 5'
R63796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 380; DB 103;
Pred. No. 0.00e+00;
0; Mismatches 8;
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                                                                                                                                                                 The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
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Best Local Similarity 97.5%;
Matches 392; Conservative
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                                                                                                                                                 Wilson, R.
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19 Gaps

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Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrini; Hominidae; Homo.
1 (bases 1 to 463)
Hillier, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High qality sequence stops: 358
Source: IMAGE Consorthium, LLN.
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
301 gigotigiggictnatacgcgagacagicccgintaggaaggccaticatgatcaaggt 360
                                                                                                                                                                                                                                                                                                                                                     human clone-150737 library-Soares placenta Nb2HP vector-pr7T3D
                                                                                                         989 GAACT-GCAGG-AGGGGCCGGAGCAGCGGGCTCCT-CGCCAAGT-GAAGCGGGCCTGCA 934
                                                                                                                                                                                                                                                              20-JUN-1995
                   gaactincagggaggggccngagcaggcnggctncttcgccaagttnaagagggcctnca
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WashIngton University School of Medicine
MashIngton University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1811.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 463;
                                                                                                                                                                                                                                                        FST 473569.s1 Homo sapiens cDNA clone 150737 3'. 99855402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 353; DB 43; L. Pred. No. 0.00e+00; O; Mismatches 11;
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94.9%;
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Matches 429; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
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AUTHORS
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Ammiota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 431)
Hiller, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lenon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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High qality sequence stops: 100
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.linl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1345 AAAATCAGTCGGGCAAAAGTTTTTCCCTACATTCTACTGTCTGATGAGATTGGAGAGCAG 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1285 CAAGAACTIGCIGICAGCAGICATITIACAAAACAGCICAGGAGGIGGGIGGCACCIAC 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1165 ATAGCAGGGCAGGCAGGGAGAGCGTCGTCTTAGTCTTGAAGAGGTCAGACACGAAGAAA 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 caagaacttgctgtcagcagtcattttacaaaacagctcaggaggtggggtggcacctac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 aaaatcagtcgggcaaaagtttttccctacattctactgtctgatgagattggagagcag 60
                                   26-MAY-1995
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                   Y115h04.s1 Homo saplens cDNA clone 139351 3'.
R63741
9835620
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Local Similarity 96.0%; Pred. No. 0.00e+00;
Nes 406; Conservative 0; Mismatches 9;
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/clone="139351"
91 c 123 q 97
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WashU-Merck EST Project
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Eukaryotae, Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Lutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 475)
Hillieri., Clark, M., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          973 GGCCCTCCTGCAGTTCACCTTGATCATGATGGCCTTCTACACGGGACTGTCTCGCGTAT 1032
                                                                                                                                                                                                                                         240
                                                                                                                                                                   61 aagtocaggaagccaggaagtocttottototggocatgootoottotocatgtacacta 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1995
                                                        Gaps
                                                                                                                  193 GCCAGATCAACTGCTGTGAAGGCTACATTCAGAACTACAGATGCAGAGGTGATGACAGCA
                                                                                            1 gocagatoaactgototgaaggotacattcagaactacagatgcagaggtgatgacanca
                                                                                                                                                                                                         853 AAGTCCAGGAAGCCAGGAAGTCCTTCTTCTCTGGGCCATGCCTTCTTCTCCATGTACACTA
                                                                                                                                                                                                                                                                                                                      ngococtcotgoagttcacottgatcatgatggccttctacacgggactgtctcgcgtat
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Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                      Length 348;
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Score 327; DB 54; Le
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
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                  24.0%;
98.0%;
                                                          Conservative
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                  Query Match
Best Local Similarity
Matches 341; Conser
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                               1165 ATAGCAGGGCAGGCAGGGAGAGCGTCGTCTTAGTCTTGAAGAGGTCAGACACGAAGAAA 1106
                                                                                                                                                                                                                                         Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 348)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                  atagcaggggcaggcaggcaggcgtcgtcttagtcttgaagaggtcagacacgaagaaa
                                                                                                                                                                                                                                                                                                                  361 gggtgaactgcaggagggccngagcaggcgggcttcctngccaagttgaagcgggcctn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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YJ49a08.rl Homo sapiens CDNA clone 152054 5'.
H04659
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/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fat: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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The WashU-Merck EST Project
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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       4444 Forest rain. ---
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
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IMAGE Consortium (info@image.llnl.gov) for further information.
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/clone_lib="Soares fetal heart NbHH19W'
Medicine
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Pred. No. 0.00e+00;
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/organism="Homo sapiens"
                                                               Insert Length: 774 Std Error:
Seq primer: mbox REGA+ET
High quality sequence stop: 336.
Location/Qualiffers
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Washington University School
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Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The WashU-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK WashU-Merck EST Project Washington University Contact: Wilson RK WashU-Merck EST Project Washington University Mo 63108 Tel: 314 286 18610 Email: Louis, Mo 63108 Tel: 314 286 18610 Email: est@watson.wustl.edu.This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. Insert Length: 774 Std Error: 0.00 Seq primer: Moo. NEGA-ET High quality sequence stop: 336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 agcaccatcaagcettaccaccgagggttttactgcaatgatgagagcatcaagtaccca
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                                                                                                                                                                                                                                  13-WAY-1996 (Rel. 47, Created)
O7-WAR-1997 (Rel. 51, Last updated, Version 2)
2C64f09-x11 Soares fetal heart NDHH19W Homo sapiens CDNA clone
327113 5' similar to WP:128D9.3 CE02068;
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (ampicillin resistant)"
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Sequence 564 BP; 128 A; 155 C; 139 G; 134 T; 8 other;
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Pred. No. 0.00e+00;
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539 atgatgggcctntacaacgggactg
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Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rikfin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The WashU-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contect: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LiLL. contact the IMAGE Consortium (infoelmage.llnl.gov) for further information: Insert Length: 774 5td Error: 0.00 Seg primer mob.REGA+ET High quality sequence stop: 312
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28-FEB-1997 (Rel. 51, Last updated, Version 2)
2c64f09.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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                                                                                                           Score 382; DB 15;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                         ctgtgc-atcagccagtctttcacagacattgccaaagtgtccatagggcgcctgcgtcc 300
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Busaryotee mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 441)
14 [lilar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hullman, M., Rucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Washu-Merck ES; Project
Unpublished (1995)
                            182 gacgattcagaacccctacgtggcagcactctataagcaagtgggctgcttcctctttgg
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Washlow Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
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/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
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JOURNAL
COMMENT
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AUTHORS
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primer:

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2P52f10.sl Stratagene HeLa cell s3 937216 Homo sapiens CDNA clone AA181403
              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 774 Std Error: 0.00
Seg primer: mob.RECA+EF
High quality sequence stop: 312.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 403;
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/lab_host="DH10B (ampicillin resistant)"
complement(<1..>403)
i 87 c 118 g 91 t 1 other:
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Pred. No. 0.00e+00;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                   /clone-"327113"
                                                                                                                                                                                                                                                                                                                                                                  /sex="unknown"
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llarity 99.0%;
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                                              normalization to a Cot - 5. Library constructed by M.Fatim
                                                                          Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHLISW." <a href="https://clone-812711">https://clone-8127111</a>
 adapters (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1287 AGCAAGAACTIGCIGICAGCAGICATITIACAAAACAGCICAGGAGGIGGGIGGCACCI 1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                                             WU2733 403 bp mRNA EST 25-NOV-1996
327113 3'.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulennan,M., Rucaba,T., Le,M., Lennon,C., Marra,M. Parsons,J., Ritkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
Har Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                         DB 87; Length 403;
                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                 /dev_stage="19 weeks" /1ab_loost="DHO08 (amplement(<1...>403) complement(<1...>403) BP: 106 A: 87 C: 118 G: 91 T: 1 other:
                                                                                                               /clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
                                                                                                                                                                                                                       Score 376; DB 87;
Pred. No. 0.00e+00;
0; Mismatches 1;
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Local Similarity 99.0%;
les 394; Conservative
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Murinae;

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US-08-842-827-5.rst2

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/organism="Mus musculus"
/note="Organ: brain; Vector: pSPORT1; Mouse Ventral
/note="Organ: brain; Vector: pSPORT1; Mouse Ventral
/note="Organ: brain; Vector: pSPORT1; Mouse Ventral
/note="Organ: brain organism 
                                                                                                                                                                                                                                                                                                                                                                            Robertson Laboratory of Biotechnology
Institute of Biomedical and Life Sciences, Division of Molecular
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                                                               Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robertson Building, 54 Dumbarton Road, Glasgow Gll 6NU Tel: 44 141 330 5102 Fax: 44 141 330 5102/4878 Email: 9pag1@dudcf.gla.ac.uk
                                                                                                                                                                          1 (bases 1 to 402)
Stewart,G.J., Savioz,A. and Davies,R.W.
Sequence analysis of 497 mouse brain ESTs expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 402;
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: gbga21@udcf.gla.ac.uk
Seg primer: T7/T3alph
High quality sequence stop: 422.
Location/Qualifiers
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1 Similarity 84.4%;
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
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307 Mouse VM cDNA library Mus musculus cDNA clone spmp22 1.22.
W39811
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 446)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E. Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 agggeteettgageaaateetgeeagaacateactgggatggtgettgtggtetgataeg
                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashUn-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Exar: 314 286 1810
Email: est@watson.wustl.edu
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 336; DB 12; Length 446 Pred. No. 0.00e+00; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
complement(<1..>446)
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Best Local Similarity 99.4%;
Matches 342; Conservative
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Source

FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS ä

1; Gaps

05-FEB-1997

RESULT LOCUS

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                       STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
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1..20
/map="981.7 cR from top of Chr2 linkage group"
/map="981.7 cR from top of Chr2 linkage group"
/map="981.7 cR from top of Chr2 linkage group"
a 109 c 147 g 128 t 14 others
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                                                                                                                                                                                                                                                                                                                Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Blomedical Research 9 Cambridge Center, Cambridge MA 02142 USA 71 1617 252 1900 Fax: 617 252 1902 Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derived from dbEST (genbank accession T71976).
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Pred. No. 0.00e+00;
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/organism="Homo sapiens"
1..150
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Primer B: TATTGACAGGAACAATCACCAC
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Polymerization:
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Template: 10 ng
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KC1: 50 mM
Tris-HCL: 10 mM
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Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer: each 5 ph
dNTPs: each 4 nM
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Best Local Similarity 98.4%;
Matches 247; Conservative
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Unpublished (1995)
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PCR Profile:
                                                                                                Homo sapiens
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                                                                            collection.
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     G13351
G1127460
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organ.sm="Mus musculus"
/organ.sm="Organ: brain; Vector: pSPORT1; Mouse Ventral
Midbrain directional cDNA library in pSPORT1. The library
was created by subtractive hybridisation using VM mRNA as
the target nucleic acid population and total cerebellar ss
cDNA as the driver nucleic acid population. The clones are
3 directed: "
/clone="spmp22 1.25"
/clone="spmp22 1.25"
/clone=lib="Mouse VM cDNA library"
/fissue_type="ventral midbrain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                          Robertson Laboratory of Biotechnology
Institute of Biomedical and Life Sciences, Division of Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1125 TICAAGACTAAGACGACGCTCTCCCTGCCTGCCCCGTGTTCGAAATCCTTTCA 1184
                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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309 Mouse VM cDNA library Mus musculus cDNA clone spmp22 1.25.
W39816
g1816979
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Pred. No. 0.00e+00;
0; Mismatches 41; Indels 1; Gaps
                                                                                                                                                                                                        the
                                                                                                                                                                1 (bases 1 to 337)
Stewart,G.J., Savioz,A. and Davies,R.W.
Sequence analysis of 497 mouse brain ESTs expressed in
                                                                                                                                                                                                                                                                                                                                             Robertson Building, 54 Dumbarton Road, Glasgow Gll 6NU Tel: 44 141 330 5102
Fax: 44 141 330 5102/4878
Email: gbga21@udcf.gla.ac.uk
Seq primer: T7/73alpb
High quality sequence stop: 337.
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Genomics 39, 147-153 (1997)
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                                                                                                                                                                                                                                                                            Contact: Davies, R.W.
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Best Local Similarity 87.4%;
Matches 291; Conservative
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DEFINITION human STS WI-12145.
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                                                                                              Mus musculus
                                                                            house mouse.
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ECORI: Site_2: Xho1; Cloned unidirectionally. Primer:
Oligo dr. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni-Zap XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This close is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 391.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL26964 421 bp mRNA EST 26-NOV-1996
2187603.s1 Stratagene colon (#937204) Homo sapiens cDNA clone
AA126964
                                                                                                                                                                                                                                                                                                                                  Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo. [ hases 1 to 421] .

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Waterston, R., Milliamson, A., Wohldmann, P. and Wilson, R. Washu-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1800
Fax: 314 286 1810
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/lab_host-"SOLR cells (kanamycin resistant)"
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Pred. No. 0.00e+00;
0; Mismatches 4; Indels
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Best Local Similarity 98.3%;
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 716 Std Error: 0.00
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                                                                                                          bp mRNA EST 25-NOV-1996 fetal heart NDHH19W Homo sapiens CDNA clone
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Hillier,L., Clark.N., Dubuque,T., Elliston,K., Hawkins,M., Hollann,M., Rucaba,T., Le,M., Lemon,G., Marra,M., Parsons,J., Rifkini.L., Rohlfing,T., Soares,M., Tan,F., Arraym., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Louis, MO 63108
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/dev_stage="lg weeks"
/lab_host="PH10B (ampicillin resistant)"
complement(<1..>374)
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. L
Tel: 314 286 1800
Fax: 314 286 1810
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High quality sequence stop: 262.
Location/Qualifiers
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Best Local Similarity 96.5%;
Matches 223; Conservative
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/note-"organ: brain; Vector: pSPORTI; Mouse Ventral Midbrain directional cDNA library in pSPORTI. The library was created by subtractive hybridisation using VM mRNA as the target nucleic acid population and total cerebellar specific as the driver nucleic acid population. The clones are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robertson Laboratory of Biotechnology
Institute of Biomedical and Life Sciences, Division of Molecular
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Vertebrata; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
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157 tittigtaaaatgactgctgacagcaagttcttgctgctccccaatctcatcagacagta 216
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308 Mouse VM cDNA library Mus musculus cDNA clone spmp22 1.23.
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/clone="spmp22 1.23"
/clone=lib="Mouse VM cDNA library"
/tissue_type="ventral midbrain"
<1..>242
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Stewart, G.J., Savioz, R. and Davies, R.W.
Sequence analysis of 497 mouse brain ESTs
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Pred. No. 2.04e-260;
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larity 89.6%;
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/clone_127811"

/clone_11b="Soares fetal heart NbHH19W"
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                     tttttgtaaaatgactgctgacagcaagttcttgctgctctccaatctcatcagacagta
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Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trewaskis E., Waterston R., Williamson A., Wohldmann P., Wilson
"The WashU-Merck EST Project";
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fetal heart NDHH19W Homo sapiens cDNA clone
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 4.06e-296;
0; Mismatches 7; Indels
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/lab_host="Pallos (ampicillin resistant)"
complement(<1..>374)
BP: 102 A; 91 C; 73 G; 101 T; 7 other;
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09-MAY-1996 (Rel. 47, Created)
07-MAR-1997 (Rel. 51, Last updi
2C71h10 sl Soares fetal heart
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Matches 223; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewaton.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 91.
                                                                                            24-FEB-1997 (Rel. 51, Created)
24-FEB-1997 (Rel. 51, Last updated, Version 1)
2p52f10.rl Stratagene HeLa cell 83 937216 Homo sapiens CDNA Clone 613099 5' similar to TR:G1161100 G1161100 HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK WashU-Merck EST Project Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                            Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Barsons J., Rifkin L., Rohlfing T., Tan F., Trevaskis E.,
Waterston R., Williamson A., Wohldmann P., Wilson R.;
"WashU-Merck EST Project";
                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.1%; Score 179; DB 81; Length 236; Best Local Similarity 91.1%; Pred. No. 8.22e-242; Matches 216; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                          standard; RNA; EST; 236
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                                                                                                                                                                                                                                                               Homo sapiens (human)
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AA182434 236 bp mRNA EST 07-JAN-1997 2p52110.rl Stratagene HeLa cell 83 937216 Homo sapiens cDNA clone 613099 5' similar to TR:G11100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN ;

AA182434

ACCESSION

15

RESULT

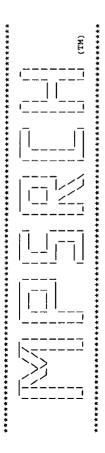
DEFINITION

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5
                                                                                                                                                                                                                                            Contact: Wilson RK
WashU-Merck EST Project
Washington Oniversity School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 91.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tontgagtgtctnaaccctgatttnaagccagattaacttgctctgaaggctacatnca 179
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
I (bases 1 to 236)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,A., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ttcagaacccctacgtggcagcactctataagcaagtgggctgctncntctttggctgt- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAACT-ACAGAIGCAGAGGIGAIGACAGCAAAGICCAGGAAGCCA-GGAAGICCTIC 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Stratagene HeLa cell s3 937216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female"
/dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 179; DB 12; I Pred. No. 8.22e-242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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91.1%;
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nes 216; Conservative
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human.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Nov 4 10:27:48 1997; MasPar time 7.48 Seconds 511.387 Million cell updates/sec

rabular output not generated.

Title: >US-08-842-827-6
Description: (1-311) from US08842827.pep
Perfect Score: 2326

refrect Score: 1226 Sequence: 1 MONYKYDKAIVPESKNGGSP......RKEILSPVDIIDRNNHHNMM 311

Scoring table: PAM 150 Gap 11 Searched: 101610 seqs, 12294212 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-

a-geneseq28 l:partl 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21

Statistics: Mean 33.923; Variance 140.094; scale 0.242

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query	Query Match Length	DB	ID	Description	Pred. No.
	111	4.8	352	20	W01663	p(H218), G-protein co	7.64e-01
7	111	4.8	352	디	R58712	Fragment of receptor	7.64e-01
£,	110	4.7	251	21	W20277	H. pylori surface or	9.15e-01
4	96	4.1	111	11	R57067	Human serotoninergic	1.07e+01
S	92	4 1	492	~	R11360	Glucose Transporter P	1.27e+01
φ	92	4.1	836	17	R87153	Alternatively spliced	1.27e+01
7	95	4.1	836	1	R58912	Product of alternativ	1.27e+01
60	95	4.1	904	17	R87147	Protocadherin clone 4	1.27e+01
6	95	4.1	904	11	R58907	Human protocadherin-4	1.27e+01
10	6	4.0	370	급	R57066	Murine serotoninergic	1.78e+01
11	06	3.9	583	20	W06891	Human activated leuko	2.94e+01
12	06	3.9	583	18	R97230	Stem cell marker HCAP	2.94e+01
13	83	9.8	263	4	R25424	Human MIP.	3.47e+01
14	83	3.8	370	13	R58686	Rat MR22 serotonin re	3.47e+01
15	88	3.8	588	13	W05297	Esterase secretory pr	4.10e+01
16	86	3.7	88	19	R90991	Mouse Mat-8 polypepti	5.69e+01
17	. 87	3.7	121	2	W20696	H. pylori secreted or	4.83e+01
18	87	3.7	216	12	R75902	Human olfactory recep	4.83e+01
19	87	3.7	357	σ	R45847	Murine 5HT5a serotoni	4.83e+01
20	96	3.7	357	12	R58685	Rat REC17 serotonin r	5.69e+01

6.70e+01 4.83e+01 6.70e+01 6.70e+01	6.70e+01 7.87e+01 9.25e+01 9.25e+01	9.25e+01 9.25e+01 9.25e+01		7.87e+01 9.25e+01 9.25e+01 9.25e+01	9.25e+01 9.25e+01 9.25e+01 1.09e+02
5HT5a sero lori transm ixin derive	A2058 autotaxin prote MHC polypeptide HLA D Human proteosome subu Human somatostatin re Murine somatostatin re	Human somatostatin re Octopus rhodopsin mem Stem cell marker HCAP Human calcium channel	1245 prot lus thuri toxin HD8 lus thuri	B.t. toxin HD511. Human neuronal calciu Human neuronal calciu Calcium channel alpha	Deduced protein seque Full length T4 encode Virulence gene cluste Lipase encoded by rec
R45848 W20661 R86578 R86595	R86596 R74037 W11860 R39261 R39262	R97269 R12362 R97231 R27648	R06461 R46226 R37214 R46225	R37213 R71009 R71010 R69604	R07640 R04031 R97245 R06606
12 16 16	7 7 20 7 4 7 4 7 4 4 4 4 4 4 4 4 4 4 4 4 4 4	183	70/0	14 14 13	1355
357 377 829 849	915 229 324 369	920	1138 1138 1138 1138	1138 2251 2270 2270	2458 2458 4472 368
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223	2 2 2 2 2 5 5 5 6 5 6 5 6 5 6 5 6 6 6 6	33 33 33 33 33 33	34 37 37	338 8 4 4 1 0 0 1	4444 0.6.40

ALIGNMENTS

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Proliteration anotor uniterentiation.

Totalm 1: Column 17-20; 33pp; English.

Claim 1: Column 17-20; 33pp; English.

This sequence is a novel rat protein p(H218), a member of the G-protein coupled receptor (GPR) superfamily of proteins. Several features of for the G-protein sequence for North and including; (1) seven regions of hydrophobicity which are predicted to act as membrane spanning domains: (1i) a consensus sequence for Northe divocayllation in the predicted condition and several serine and threonine residues in its predicted C-terminal domain. In addition, p(H318) contains many other residues which are condition in that it does not contain certain highly conserved residues. Perhaps most notable are the aspartate and tyrosine residues at the contain certain highly conserved residues. Perhaps most notable are the aspartate and tyrosine residues at the cytoplasmic end of the third transmembrane domain, and the cysteine residue at the extracellular end of the same transmembrane domain. The amino acid similarity between p(H218) and p(rat-edg) (W01664) suggests.
                                   W01663;
01-APR-1997 (first entry)
0F(H218), G-protein coupled receptor.
0F(H218); G-protein coupled receptor; cell differentiation, proliferation;
0F(H218); G-protein coupled receptor; cell differentiation, proliferation;
prolline directed kinase; cell division; growth factor response; rat-edg;

    associated with cell

                                                                                                                                                                                                                                                                                                                                                                        /note= "consensus sequence for proline directed
                                                                                                                                                                                                                                 /note- predicted N-glycosylation site"
Binding_site 222..225
'note- possible nucleotide binding site"
Binding_site 309..315
/note- possible nucleotide binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding rat protein p(H218) - as
proliferation and/or differentiation
                                                                                                                                                                                        Location/Qualifiers
                W01663 standard; Protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                              Misc_difference 342..343
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-1994; 196989.
15-FEB-1994; US-196989.
(MACL/) MACLENNAN A J.
                                                                                                                                                therapy; diagnosis.
Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 97-051235/05.
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                                                                                                                                                                                                                Modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maclennan AJ;
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US5585476-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-1996
RESULT
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compound; bacterium; life cycle; activator; bacteria; inhibitor;
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                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                          Smith D,
                                                          06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-1994; F00136.
09-FEB-1993; FR-001392.
                           Helicobacter pylori. WO9640893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 94-279740/34.
N-PSDB; Q70265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AA:
                                                                                                         Berglindh OT, Smi
WPI; 97-052306/05.
                                                                                               (ASTR ) ASTRA AB.
                                                                                                                               N-PSDB: T67487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                  19-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                               Sequence
                duodenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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that they may be activated by the same endogenous ligand(s). The expression pattern of mRNA transcripts of both genes in cell lines, various rat tissues and developing rat brain suggests that they both play a role in cell proliferation and/or differentiation. Sequence 352 AA;
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                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W20277;
09-701-1997 (first entry)
H. Pylor surface or membrane protein, 23945317.aa.
Cytoplasmic; vaccine; prevention; treatment; infection; identification;
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence encodes a fragment of the GTP-binding receptor which contains all seven transmembrane domains. The receptor protein occurs to the greatest extent in heart and lung tissue and to a lesser extent in the stomach and intestines. The peptide is therefore useful in the design and screening of candidate drugs, especially for the cardiovascular system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor peptide for GTP-binding protein - can be used as a tool in design and screening of cardiovascular drugs Claim 2; Page 16-18; 27pp; Japanese.
                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                         05-APR-1995 (first entry)
requent of receptor for GTP-binding protein.
Receptor; GTP: binding protein; heart; lung; cardiovascular;
screening; testing; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 4.8%; Score 111; DB 11; Length 352; Local Similarity 37.8%; Pred. No. 7.64e-01; les 17; Conservative 8; Mismatches 19; Indels
                                                                       Length 352
                                                                     Score 111; DB 20; Length 35 Pred. No. 7.64e-01; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 vlcvvtífsvillaivalyvríyfvvrsshadvagpqtlallktv 235
                                                                                                                                      87 VLCAVGIVIAILAIITGEFYRIYYL-KKSRSTIQNPYVAALYKQV 130
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                        л 2
R58712 standard; Protein; 352 АА.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W20277 standard; protein; 251 AA.
                                                                                                                                                                                                                                                                                                                                                Domain 148..173 //label = Transmembrane domain.
                                                                                                                                                                                                                                                                              Jomain 35.59
                                                                                                                                                                                                                                                                                                              /label- Transmembrane domain.
Domain 110..128
                                                                                                                                                                                                                                                                                                                                     /label= Transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                /label- Transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                      /label- Transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                           /label- Transmembrane domain.
WO9418237-A.
                                                                     Query Match 4.8%;
Best Local Similarity 37.8%;
                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                      190..210
                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1994.
10-FEB-1994; J00202.
10-FEB-1993; JP-044330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TSUR ) TSUMURA & CO.
Takuwa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 94-279690/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAKU/) TAKUWA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q71655
                                                                                                                                                                                                                                                        Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Domain
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polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Halicobacter Claim 73; Page 479; 1481pp. English.

Claim 74; Page 479; 1481pp. English.

Claim 75; Page 479; 1481pp.

Claim 75; Page 479; 1481pp.

Claim 75; Page 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-WAR-1995 (first entry)
Human serotoninergic receptor SHTSb.
Serotoninergic receptor SHTSb; 5-hydroxytryptamine; neuromodulator;
mouse serotonin receptor; neurological; cardiovascular; psychiatric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Claim 5; Page 18; 27pp; French.
A human placental genomic DNA library was screened with the mouse
serotoninergic receptor 5HT5b CDNA (070264). A sequence coding for
the human 5HT5b receptor was identified (070265).
ulcer disease; chronic gastritis; diagnosis; envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant cells - useful for treatment and diagnosis of e.g. neurological or cardiovascular disease, also for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori nucleic acid sequences and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plassat
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Best Local Similarity 23.3%; Pred. No. 9.15e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Amlaiky N, Boschert U, Hen R, Matthes H, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 fisifs-salf-cfclaifvarifqneqsi 164
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256 VLAGFAQGALVAC-CIVFFVSDLFKTKTTL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mellgaerd BL;
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Purply 1003cs.

Purply 1003cs.

Purply 1003cs.

Purply pc5 - involved in cell-cell adhesion and regulation activities

Example 3; Page 100-104; 146pp; English.

Example 3; Page 100-104; 146pp; English.

RN 1153 and RB 7154 represent possible alternatively spliced versions of the clone of the human protocadherin sequence, designated po43. The CDNA conciling these sequences were isolated after screening a human foetal brain cDNA library (contained within lambda2apil vectors), with 32P labelled versions of the sequences represented by T03605 and T03606. The most abundant spliced version of po43 is represented in T03622. The cytoplasmic domain of cadherin interacts with the cytoskeleton through cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adherive function. The cytoplasmic domain appear to function via a different nethose with a cytoplasmic domain. These protein sequences are involved in cell-cell adhesion. This sequence may have regulatory functions in the cell, as well as the cell-cell adhesive properties.

Antibodies produced against these sequences are useful for modulating the binding activity of protocadherins, and can be used therapeutically.

Sequence 836 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No Purple Cookering and regulating activities.

Example: Page 96-99: 114pp; English.

Two full length human cDNAs corresp. to the partial cDNAs of From human fetal brain cDNA library. Several overlapping cDNA clones were isolated with each probe including two cDNAs which contained the putative entire coding sequences of two novel professions designated protocadherin-42 (pc43) and protocadherin-43 (pc43). The DNA and deduced AA sequences of pc42 are in Q68997/R88906, while those of pc43 are in Q68998/R88907. Sequence clones contd. unique sequences at the 3' end. The analysis of various overlapping protocadherin cDNA clones revealed that some clones contd. unique sequences at the 3' end. The sequences forming the boundaries of the 3' end regions are consistent with the consensus sequence of mRNA splicing, suggesting the DNA and AA sequences of tone possible product of alternative splicing of pc42 mRNA are respectively presented in Q68909/R58911. The DNA and AA sequences of two possible products of alternative splicing of pc42 mRNA are respectively presented in Q68900/R58912 and Q69001/R4914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.7-APR-1995 (first entry)
Product of alternative splicing of human protocadherin-43 mRNA.
Cadherin; protocadherin; cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 4.1%; Score 95; DB 17; Length 836; Local Similarity 33.3%; Pred. No. 1.27e+01; es 15; Conservative 15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 4.1%; Score 95; DB 11; Length 836
Best Local Similarity 33.3%; Pred. No. 1.27e+01;
Matches 15; Conservative 15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       698 ilvsvgfvvtvfgvii--f-kvykwkqsrdlyrap-vsslyrtpg 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 ilvsvgfvvtvfgvii--f-kvykwkqsrdlyrap-vsslyrtpg 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R58912 standard; Protein; 836 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DOHE-) DOHENY EYE INST
Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-998003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1993; U12588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 94-293849/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q69000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9414960-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Alternatively spliced pod3 *1.
Protocodherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse; catenin; therapy; clone; frog; fruit fly.
Homo saptens.
W09600289-Al.
04-JAN-1996.
27-JUN-1996, US-268161.
CDOHE.) DOHENY EYE INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transfecting eukaryotic cells with a replicable vector -
comprising nucleic acid sequence encoding a GTP operably linked
recomprising nucleic acid sequence encoding a GTP operably linked
to control sequences recognised by transfected cells
claim 27; Fig 11; 58pp; English

A CDNA library was prepared in lambda gt10 from total cellular RNA
Cfrom CHO-FR4 cells. The library was screened with 3 probes (see
Cli149-C01151) based on highly conserved regions of the known rat
and human facilitative GTP sequences. One positive plaque was
identified (out of 150000), replated and screened with 2 of the 3
probes. Phage DNA was prepared from one of the positive plaques and
its 2.5kb cDNA insert excised using EcoRI. The insert was ligated
into PRKS and transformed into E.coli strain SRAIO! Recombinant
clones were picked for sequencing. The complete GTP-encoding
sequence was used to transform eukaryotic cells to allow them to be
fatty acids, metal lons, transferrin, serum and insulin.
Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 ynqtwvhrygepivpttlttlwslsvaifsvggmigsfsvglfvn-rfgrrnsmlmmnll 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 YIQNYRCRGDDSKVQEARKSFFS-GHASFSMYTWL--YLV-LYLQARFTWRGARLLRPLL 230
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                            5
                                                                                                                          248 DHKHHPSDVLAGFAQGALVACCIVFFVSDLFKTKTTLSLPAPAIRKEIL 296
                  Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 95; DB 2; Length 492;
Pred. No. 1.27e+01;
18; Mismatches 26; Indels
                                                                                                 31 eqkerraammvgiligvfvlcwipffltelisplcacslp-p-iwksif 77
                Score 96; DB 11; Length 111 Pred. No. 1.07e+01; 15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                     04-JUN-1991 (first entry)
Glucose Transporter Protein from CHO cells.
GTP; serum-independence; Chinese Hamster Ovary;
Hanlin-independence.
                                                                                                                                                                                           .T 5
R11360 standard; Protein; 492 AA.
R11360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R87153 standard; Protein; 836 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.6%;
Matches 20; Conservative
             Query Match 4.1%;
Best Local Similarity 32.7%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     28-ACG-1990; UO4849,
01-SEP-1989; US-402204,
20-UUN-1990; US-541426,
(GETH ) GENENTECH INC.
Thomas JN, Williams SR;
WPI; 91-102073/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 afvsavlmgf 112
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                                                                                                                                                                                                                                                                                                                                                           Cricetulus sp. W09103554-A.
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                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1991
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Length 836;

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 94-279740/34.
N-PSDB; Q70264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynuclectide(s) encoding human protocadherins pc3 and pc4 and rat polynuclectide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities
Example 3; Page 79 84; 146pp. English.

This sequence represents a clone of the human protocadherin sequence, designated pc43. The CDNA encoding this sequence was isolated after careening a human foetal brain cDNA library (contained within lambdazapil crectors), with 32P labelled versions of the sequences represented by T0360s and T0360s. The cytoplasmic domain of cadherin interacts with the cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function.

The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain.

This protein sequence is involved in cell-cell adhesion. This sequence may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against this sequence are useful for modulating the binding activity of protocadherins, and can be
                                                                                                                                                                                                  rat; cadherin; cell adhesion; mouse; fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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N-F5DB, 08898.
Polynclectide sequences encoding new proto:cadherins - useful
for modulating natural binding and regulating activities.
Claim 14; Pege 78-81; 114pp; English.
Two full length human cDNAs corresp. to the partial cDNAs of
HUMAN-42 and HUMAN-43 (06898, 068982) were isolated
from human fetal brain cDNA library. Several overlapping cDNA
clones were isolated with each probe including two cDNAs which
contained the putative entire coding sequences of two novel
proteins designated protocadherin-42 (pc42) and protocadherin-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15, Mismatches 11; Indels
698 ilvsvgfvvtvfgvii--f-kvykwkqsrdlyrap-vsslyrtpg 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cadherin; protocadherin; cell adhesion molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ş
                                                                                                                                                                                                       Protocadherin; pc3; pc4; pc5; human; catenin; therapy; clone; frog; fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R58907 standard; Protein; 904 AA.
                                                                                                                 Ą
                                                                                                              standard; Protein; 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.3%;
Matches 15; Conservative
                                                                                                                                                      29-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DOHE-) DOHENY EYE INST.
Suzuki S;
                                                                                                                                                                                                                                                                                                                                                             DOHE-) DOHENY EYE INST
                                                                                                                                                                                 Protocadherin clone 43.
Protocadherin; pc3; pc4
                                                                                                                                                                                                                                                                                           04-JAN-1996.
26-JUN-1995; U08071.
27-JUN-1994; US-268161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUL-1994.
23-DEC-1993; U12588.
29-DEC-1992; US-998003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protocadherin-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for modulating used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                              96-068873/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 94-293849/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T03622
                                                                                                                                                                                                                                                   Homo sapiens.
WO9600289-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9414960-A.
                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                            R87147
                                                                                                                                                                                                                                                                                                                                                                                        Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R58907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine serotoninergic receptor 5HT5b.
Serotoninergic receptor 5HT5b; 5-hydroxytryptamine; neuromodulator;
mouse serotonin receptor; neurological; cardiovascular; psychiatric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serotonin agonists and antagonists
Claim 1; Pages 17-18, 27pp; French.
Clidim 1; Pages 17-18, 27pp; French.
Serotonin receptors were used in PCR of mouse brain RNA in presence
of reverse transcriptase and the products were sequenced. One
product with homology to known receptors was labelled and used to
probe a CDNA library in Lambda UnizAP. The 2036 bp sequence 070264
domains which represents a novel serotonin receptor which was
designated 5HTSb (RS7066).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
(pc43). The DNA and deduced AA sequences of pc42 are in 06899/R58906, while those of pc43 are in 06899/R58907. The overall structures of pc42 and pc43 are similar to that of that overall structures of pc42 and pc43 are similar to that of typical cadherins but they do have distinct features. Both lack the prosequences that are present in all known cadherin precursors. The extracellular domains of pc42 and pc43 are different in length and pc42 contains seven subdomains that closely resemble the typical cadherin extracellular subdomain while pc43 has six such those of known cadherins or cadherin-related proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New serotoninergic receptor 5HT5b and related nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human activated leukocyte-cell adhesion molecule ALCAM.
Activated luckcyte-cell adhesion molecule; ALCAM; CD6 ligand;
thymic epithelial cell; inflammation; allograft rejection;
neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant cells - useful for treatment and diagnosis of e.g. neurological or cardiovascular disease, also for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95; DB 11; Length 904; Pred. No. 1.27e+01; 15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 eqkekraammvgiligvfvlcwipffltelisplcacslp-p-1wksif 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 DHKHHPSDVLAGFAQGALVACCIVFFVSDLFKTKTLSLPAPAIRKEIL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DB 11; Length 370; Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     698 ilvsvgfvvtvfgvii--f-kvykwkgsrdlyrap-vsslyrtpg 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Amhaiky N, Boschert U, Hen R, Matthes H, Plassat Grailhe R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .T 10
R57066 standard; Protein; 370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .r 11
W06891 standard; Protein; 583 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Match
Local Similarity 32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Conservative
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R25424 standard; Protein; 263 AA.
                                                                                                                                                                                                                                                                                  T 12
R97230 standard; Protein; 583 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYST-) SYSTEMIX INC.
Gearing D, Uchida N, Yang Z;
WPI; 96-269990/28.
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Modified_site 231
/note-"phosphorylation site"
Modified_site 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "consensus sequence"
ed_site 229
                                                     Query Match
Best Local Similarity 42.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.9%;
Best Local Similarity 42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LZ-JUN-1995.
02-FEB-1995; 300661.
06-DEC-1994; US-352323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 AA;
       583 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T28819
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Modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUN-1996
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                  R97230;
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                                                                                                                                                                                                                                                                                                            The figure of the first of the 
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WPI; 96-506097/50.
N-PSDB; 146075.
                                                                                               Domain
/label- Extracellular_domain
/note- "the extracellular doamin can be subdivid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // Albel - Asn. Ser
/note= "variation owing to polymorphism in HL60
and T-cell derived clones"
and fied site 265
/label Glycosylation
/note= "putative N-glycosylation site"
Misc_difference 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label-Met, Thr
/note-"variation owing to polymorphism in HL60
and T-cell derived clones"
Modified_site 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Glycosylation
/note= "putative N-gklycosylation site"
                                                                                                                                                                                                                                                                                                                                                          Modilec_s.c.
/label= Glycosylation
/note= "putative N-glycosylation site"
...attion site 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Glycosylation
/note= "putative N-glycosylation site"
                                                                                                                                                                                                                                                                                          /label= Glycosylation
/note= "putative N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Glycosylation
/note- *putative N-glycosylation site*
Wodified_site 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label Glycosylation
'note "putative N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Glycosylation
/note= "putative N-glycosylation site"
Misc_difference 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-1996.
29-ARR-1996.
01-MAY-1995; US-432016.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
(UYDU-) UNIV DUKE.
                                                                                                                                                                                                  'label- Transmembrane_domain
                                                                                                                                                                                                                                                     'label- Extracellular_domain
                                          label Mat_protein
Peptide
/label= Sig_peptide
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human haematopoietic cell antigen proteins - useful as stem cell marker proteins in functional studies and for antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 4A; 17pp; English. However the control of 1897230 and HCAPFO.1 (1897231) are novel human haematopoietic cell antiqens associated with stem cells. They are the respective products of nucleic acid sequences HCASeq.1 (178819) and HCASeq.2 (178819) and HCASeq.2 (178819) and HCASeq.2 (178810) obtains and HCASeq.2 (178810) as tem cell marker proteins. The proteins are useful as stem cell marker proteins in functional studies, and can also be used to produce antibodies that allow the purification of stem cells from haematopoietic and other sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Major intrinsic protein; vertebrate; lens fibre membrane; cell; communication; differentiation; cateracts; uveitis; mapping. Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                     08-0CT-1996 (first entry)
Stem cell marker HCAPro.1.
Stem cell marker; haematopoietic cell antigen; HCA; HCASeq.1;
                             Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90; DB 18; Length 583; Pred. No. 2.94e+01; 13; Mismatches 5; Indels
Score 90; DB 20; Length 383.
Pred. No. 2.94e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 ekvndgakl-ivgivvglllaalvagvvywly-mkkskta 557
                                                                                                                                  520 ekvndqakl-ivgivvglllaalvagvvywly-mkkskta 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key Modified_site 177, hote" N-glycosylation site" Binding_site 225. 241 /note" "calmodulin binding site" 179. 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Modified_site 245
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label- kinase C phosphorylation site
                                                                                                                                                             N-PSDB; 072270
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                                                                                                                                     Erlander MG,
                                                                                  39-SEP-1994.
                                                                     WO9421670-A
                                                                                                                                                                                                    pathologies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-1996
                                                        /label=
                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Major intrinsic protein gene prod. - used to detect cataracts and major intrinsic protein gene prod. - used to detect cataracts and bisclosure; Fig 7, 51pp; English.

DNA encoding it used as probe for human genome
Disclosure; Fig 7, 51pp; English.

The MIP sequence was deduced from the human MIP DNA sequence obtd. by screening ca. 500,000 recombinant phage plaques from a human genomic library in EMBL-3 with a bovine CDNA fragment contig. nearly the entire MIP gene coding sequence. MIP is specifically located in the lens fibre membrane of vertebrates and may play a role in lens fibre cell communication. MIP serves as a marker of lens fibre cell fibre cell communication in that its expression is developmentally regulated. Thus, anti-MIP antibodies can be used in an immunoreaction to be used for diagnosis of autoimmune diseases, i.e. uveitis. MIP DNA probes may be used in the mapping of the human genome. The human genome. The human genome and may be used in gene therapy to target the expression of any desired gene to the fibres of the ocular lens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat MR22 serotonin receptor protein.
Serotonin; receptor; transmembrane; domain; kinase; phosphorylation;
Serotonin; receptor; transmembrane; domain; kinase; phosphorylation;
sensor; motor; behaviour; central nervous system; CMS; superfamily;
G-protein; ligand-gated; ion channel; subfamily; human; rat; amplify;
primer; PCR; amplification; brain; hypothalamus; indolamine; drug;
hypothalamus; therapeutic; neurological; pathology; dementia; insomnia;
Parkinson's disease, eating disorder; anxiety; migraine; headache.
                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                        3 elrsasfw-raifaeffatlfyvffglgsslrwapgplhvlqvamafglalatlvqsvgh 61
                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  29; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                          Length 263;
                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.8%; Score 89; DB 4; Le Best Local Similarity 22.0%; Pred. No. 3.47e+01; Matches 18; Conservative 29; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- transmembrene domain
Modified_site 163
/label- kinase C phosphorylation site
Modified_site 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= transmembrane domain
Modified_site 272
/label= kinase C phosphorylation site
Modified_site 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R58686 standard; Protein; 370 AA.
R58686;
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                         25-FEB-1992.
30-APR-1991, 250292.
30-APR-1991, US-693291.
(USSH ) US DEPT HEALTH & HUMAN.
Plsano MM, Chepelinsky AB;
WPI; 92-123644/15.
N-PSDB; Q22501.
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'note- "phosphorylation site"
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Caim 6; page 142-143; 188pp; English.

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The amino acid sequence of the novel rat serotonin receptor MR22. The amino acid sequence of the novel rat serotonin receptor solicins of the amino acid sequence of the novel rates.

The amino acid sequence of the novel rat serotonin receptors are foreign as the entral carge of sensory, motor and behavioural functions in the central carvous system (UNS).

Serotonin receptors belong to at least two protein suptemblishes: G-protein - associated receptors containing 7 TMDs (S-TTIA). The serotonin receptors presented in the patent represent prototypes that fall into three new serotonin subfamily classifications: 5-HTIG-like (rat MR77 - 07227) and 5-HTIG-like (rat MR77 - 07227) and 5-HTIG-like (rat MR77 - 07227) and 5-HTIG-like (rat MR77 - 07228) and 5-HTIG-like (rat MR77 - 07228) and 5-HTIG-like (rat MR77 - 07228) and 5-HTIG-like (rat MR77 - 07227).

SHTS (subdivided into 5-HTIG-like (rat MR77 - 07228) and 1-HTIG-like (rat MR74 - 07228) and 1-HTIG-like
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Esterase secretory protein (ORF1 product).
Esterase secretory gene; protein secretion.
Serratia marcescens strain Sr41 (FERM BP-487).
EP-733707-A2.
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Akatsuka H, Kawai E, Shibatani T;
WPI; 96-444599/45.
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W05297 standard; Protein; 588 AA.
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15-MAR-1993; US-031538.
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23-MAR-1995; JP-063772.
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increase the productivity and extracellular secretion of esterases
                   Claim 3; Page 15-17. 29pp; English.

3 Different proteins (W05297-99) participate in the mechanism of secretion of esterase by Serratia marcesens ST41. They are encoded by an esterase secretory gene (T39662) that includes 3 open reading frames. The proteins can be produced by transformed host cells, pref. S. marceseens or E. coll, carrying wencor plasmids incorporating the esterase secretory gene. The esterase is secreted from the host cell, and is recovered from the culture medium and from within the cells. The esterase is useful in hydrolysis reactions.
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э ; 4; Gaps Score 88; DB 19; Length 588; Pred. No. 4.10e+01; 19; Mismatches 33; Indels Query Match 3.8%; Best Local Similarity 23.3%; Matches 17; Conservative

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61 ltlimlgmfgmms 73 :||||: : :| 232 FTLIMMAFYTGLS 244

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Nov 4 10:26:08 1997; MasPar time 11.72 Seconds 766.881 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-842-827-6 (1-311) from USO8842827.pep 2326 1 MQNYKYDKALVPESKNGGSP......RKEILSPVDIIDRNNHNMM 311 Title:

Description: Perfect Score: Sequence:

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91006 seqs, 28888923 residues Searched:

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Mean 45.794; Variance 101.235; scale 0.452 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Query Match Length	DB	а	Description	Pred. No.
-	187	8.0	274	===	569561	hypothetical protein	2.09e-12
7	167	7.2	289	Π	870114		1.976-09
m	138	5.9	216	10	832217		2.46e-05
4	128	5.5	157	7	558067	probable olfactory r	5.33e-04
S	122	5.2	185	14	528996	G protein-coupled re	3.20e-03
ø	120	5.2	1571	디	820669	hypothetical protein	5.75e-03
7	118	5.1	239	12	564327	probable membrane pr	1.03e-02
æ	111	4.8	180	14	E48909	G-protein coupled re	7.57e-02
σ	111	4.8	352	14	JC1465	probable G protein-c	7.57e-02
10	112	4.8	409	S	526033	NADH dehydrogenase (5.72e-02
7	109	4.7	157	13	S57995	probable olfactory r	1.32e-01
12	66	4.3	236	16	151740	MHC class II alpha c	1.94e+00
13	66	4.3	236	16	151745	MHC class II alpha c	1.94e+00
7	66	4.3	236	16	151741	MHC class II alpha c	1.94e+00
12	101	4.3		12	S49959	probable membrane pr	1.15e+00
16	101	4.3	381	80	524611	latent membrane prot	1.15e+00
17	101	4.3	404	ထ	S21660	latent membrane prot	1.15e+00
18	101	4.3	404	4	LABECA	latent membrane prot	1.15e+00
13	101	4.3	529	13	S12787	potassium channel pr	1.15e+00
20	66	4. A	595	10	E64460	hypothetical protein	1.94e+00
71	101	4.3	1612	11	S51243	probable ATPase (EC	1.15e+00

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#formal_name Bacillus megaterium
06.Feb-1995 #sequence_revision 06.Feb-1995 #text_change
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                               Fulton, L. submitted to the EMBL Data Library, May 1996 The sequence of S. cerevisiae cosmid 9819. 870114
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Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, submitted to the EMBL Data Library, July 1995
Male germ cells from several mammalian species express a specific repertoire of olfactory receptor genes.
558067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor (clone PTE01) - rat (fragment) #formal_name Rattus norvegicus #common_name Norway rat 22-Nov-1993 *sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 llvflsilisllvsglhnsvvlgltyfksvdishffc-dpslllnlacsdtftnnivmyf 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abe, K.; Kusakabe, Y.; Tanemura, K.; Emori, Y.; Arai, S. FEBS Lett. (1993) 316:253-256
Multiple genes for G protein-coupled receptors and their
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                                                                                                                                                                                                                                                                                                                                                                                                           35 LLICLD-LFCLFMAGLP-FLIIETSTIKPYHRG-FYCNDESIKYPLKTGETI-NDAVLCA 90
                                                                                                                                                                                                                                                                                                                    Gaps
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28-May-1993 #sequence_revision 24-Feb-1995 #text_change
03-May-1996
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hypothetical protein YER166w - yeast (Saccharomyces cerevisiae)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 122; DB 14; I
Pred. No. 3.20e-03;
30; Mismatches 32;
                                                                                                                                                                                                                                                                 Score 128; DB 14;
Pred. No. 5.33e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 vgtisgflp1-sgiffs-yy-kivssilrmpspggkyk 111
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Y #length 157 #checksum 1240
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#length 185 #checksum 2049
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##cross-references EMBL:U18922
                                                                                                                                                                    1-157 ##label VAN
                                                                                                           ##molecule_type mRNA
##residues
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Best Local Similarity 27.6%;
Matches 27; Conservative
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Local Similarity 28.6%;
nes 28; Conservative
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329,330,331,332
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190-210
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272-293
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Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.;
Komp, C.; Wel, Y.; Taylor, P.; Nakahara, K.; Roberts, D.;
                                                                                                                                                                                                                                                                       1244 vndtislvvpqlyrvgilrkewnqrkflwymldglyqsiicififpylvyhknmivtsngl 1303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 TWRGARLL-RPLIQFTLIMMAFYTGLSRVSDHKHHPSDVLAGFAQGALVACCIVFFVSDL 277
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#domain transmembrane #status predicted #label TMZ\
#domain transmembrane #status predicted #label TM3
#length 239 #molecular-weight 27649 #checksum 3184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              rerevisiae)
hypothetical protein G4085
#formal_name Saccharomyces cerevisiae
#formal_loame Saccharomyces cerevisiae
17-May-1996 #text_change
19-Jul-1996
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21; Mismatches 22; Indels 2;
                                               Davis, R.W. submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                           Length 1571;
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                                                                                                                                                                                                       Score 120; DB 11; Length 15
Pred. No. 5.75e-03;
29; Mismatches 40; Indels
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                                                                                                           ##residues 1-222 ##label MUL
##cross-references EMBL:L10718
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llarity 20.0%;
Conservative
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Best Local Similarity 27.4%;
Matches 17; Conservative
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Matches 18; Conserv
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Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.; Jenkins, N.A. Genomics (1993) 18:175-184 at a decenders (1993) 18:175-184 at a decenter of mammalian G-protein-coupled receptors.
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#domain transmembrane #status predicted #label TM2\
#domain transmembrane #status predicted #label TM3\
#domain transmembrane #status predicted #label TM5\
#binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JC1465 #type complete probable G protein-coupled receptor - rat #formal_name Rattus norvegicus #common_name Norway rat 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -
Caenorhabditis elegans mitochondrion (SGC4)
#formal_name mitochondrion Caenorhabditis elegans
12.Feb-1993 *sequence_revision 12-Feb-1993 *text_change
10-Sep-1994
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#binding_site phosphate (Thr) (covalent) #status
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                                                                                                                                                                                                      preliminary; nucleic acid sequence not shown
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97

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41 LFCLFMAGLP-FLIIETSTIKPYHRG-FYCNDESIKYPLKTGET-INDAVLCAVGIVIAI
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Male germ cells from several mammalian species express a specific repertoire of olfactory receptor genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *superfamily NADH dehydrogenase (ubiquinone) chain 4 membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; oxidoreductase; respiratory chain #length 409 #molecular-weight 47206 #checksum 6596
                                                    #Journal Genetics (1992) 130:471-498
#title The mitochondrial genomes of two nematodes, Caenorhabditis elegans and Ascaris suum.
#cross-references MUID:92201655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okimoto, R.; Macfarlane, J.L.; Wolstenholme, D.R.
Nucleic Acids Res. (1990) 18:6113-6118
Evidence for the frequent use of TTG as the translation
initiation codon of mitochondrial protein genes in the
nematodes, Ascaris suum and Caenorhabditis elegans.
S26014
Okimoto, R.; Macfarlane, J.L.; Clary, D.O.; Wolstenholme,
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                                                                                                                                                                                                        the authors translated the initiation codon TTG for residue 1 as Leu
                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-15 ##label OK2
##cross.references EMBL:X34252
##note the authors translated the initiation codon TTG for
residue 1 as Leu
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#formal_name Canis lupus familiaris #common_name dog
13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
01-Mar-1996
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25; Mismatches 22; Indels
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##rosidnes 1-409 ##label OKI
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Sultmann, H.; Mayer, W.E.; Figueroa, F.; O'Huigin, C.; Klein,
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MHC class II alpha chain - Danio rerio
MHC class II alpha chain -
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
13-Sep-1996
15.3-150-1996
                                                                                                                                             151740 *type complete
MHC class II alpha chain - Danio rerio
*formal_name Danio rerio
13-Sep-1996 *sequence_revision 13-Sep-1996 *text_change
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MHC class II alpha chain - Danio rerio
#formal_name Danio rerio
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#title Zebrafish WHC class II alpha chain-encoding genes:
polymorphism, expression, and function.
#cross-references WULD:94011091
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##cross-references GB:L19445; NID:9311192; CDS_PID:9311193
Y #length 236 #molecular-weight 26136 #checksum
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##cross-references GB:L19450; NID:g311202; CDS_PID:g311203
X #length 236 #molecular-weight 26205 #checksum
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84 lpi-sgiffs-yy-kivssilrvpstggryk lll
                            Score 99;
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Sultmann, H.; Mayer, W.E.; Figueroa, F.; O'Huigin, C.; Klein,
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#domain transmembrane #status predicted #label TM4\
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#length 346 #molecular-weight 37418 #checksum 6022
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probable membrane protein YIL023c - yeast (Saccharomyces
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#formal_name Saccharomyces cerevisiae
28-May-1993 #sequence_revision 24-Feb-1995 #text_change
01-Mar-1996
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submitted to the EMBL Data Library, December 1994
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82 TINDAVLCAVGIVIAILAIITGEFYRI 108
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KEYWORDS transmembrane protein
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Search completed: Tue Nov 4 10:27:30 1997 Job time: 82 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

 n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

MasPar time 1135.34 Seconds 1317.542 Million cell updates/sec Thu Nov 6 11:36:00 1997; Run on:

Tabular output not generated.

>US-08-842-827-5 (1-1362) from US08842827.seq 1362 Perfect Score: Description: Title:

Sequence: Comp:

default TABLE Gap 6 Scoring table:

Dbase 0; Query 0 STD Mmatch

362067 seqs, 549138275 bases x Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database

1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC

genbank99

Database:

18 BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2 31:GEN3 32:HCT3 34:HTG3 34:HTG3 33:HNV1 36:LNV2 37:HNV3 38:LNV4 39:LNV2 32:HTG1 33:HTG2 34:HTG3 35:HV1 30:LNV2 37:HNV3 38:LNV4 39:LNV2 40:LNV2 40:LNV2 42:LNV2 42:LNV2 44:LNV1 40:LNV2 40:LNV2 40:LNV2 42:LNV2 40:LNV2 52:VR4 53:PAT3 56:RAT4 57:PAT5 58:PAT5 56:RAT4 57:PAT5 58:PAT6 56:PAT6 59:PAT6 59:PAT6 59:PAT6 59:PAT6 59:PAT6 59:PAT6 59:PAT7 57:PAT7 57:PAT

106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:VRT 114:PHG 115:PLN 116:PRII 117:PRIZ 118:ROD 119:SYN 120:UNA 121:VRL U-embl50.99 genbank-new3 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Variance 5.524; scale 2.114

Mean 11.681;

Statistics:

R. Norvegicus mRNA for Conceros Processors Muse musculus (2006-16) House mouse; Musculus 1:50e-56 House mouse; Musculus 1:50e-56 House mouse; from paten 6:42e-06 Sequence 5 from paten 6:42e-06 Sequence 5 from paten 1:22e-06 Rat nucleolin gene. 1:22e-00 Caenorhabditis elegan 1:22e+00 Caenorhabditis elegan 1:23e+01 Caenorhabditis elegan 1:33e+01 Synthetic DNA for pre 1:33e+01 Synthetic DNA for pre 1:33e+01 Synthetic DNA for pre 1:33e+01 BSP-bone sialoprotein 1:33e+01 BSP-bone sialoprotein 1:33e+01 Human mRNA for Neurob 1:33e+01 Human mRNA for Neurob 1:33e+01 Human mRNA for Neurob 1:33e+01 Human actic mNA for zic pr 1:33e+01 Mouse mRNA for zic pr 1:33e+01 Human calcium depende 1:33e+01 Human calcium activat 1:33e+01 Human calcium activat 1:33e+01 Adeno-associated viru Drosophila virilis mo Caenorhabditis elegan Caenorhabditis elegan Human DNA from cosmid Equine herpesvirus 2, Human DNA sequence ** Human clone 23748 mRN R.norvegicus mRNA for CELF59A6 HUM19ANON1 CEF13E6 RGU67155 CSD043316 CSD043316 HSD347 BD347 GGU67889 GGU67889 MCSSTA MWZIC HSU01717 HSU11717 HSU11717 HSU11058 AVWH 8044 HUMBMILX RATNUCIA3 MUS45SRNA CET27E9 CET28A8 CET28A8 DROGYPSYZ CEC34B7 ALIGNMENTS HSU79294 RNDRI42 D84376 DMU73822 MUSHPIP 128278 128278 RATCEAC MMHGM2 S78239 113410 A10161 A10159 GGRSFR 33 1110 1110 53 53 553 1122 1123 338 1122 1117 50 41 77 77 76 77 76 77 76 882 77 77 67 В 170789 1400 1770 1914 2170 2502 2502 2578 2760 37940 39320 Length 201 201 801 870 Match TITLE JOURNAL REFERENCE Result No. RESULT LOCUS DEFINI ACCESS NID KEYWORI SOURCE ORGAI AUTH AUTH JOUH MEDI AUTH 0000 00000 00000

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n	H20/9294	1444 DD	MKNA	PRI	30-0AN-139/
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CE	human.				
GANISM	Homo sapiens	•			
	Eukaryotae;	mitochondria	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	fetazoa; Ch	ordata;
	Vertebrata;	Eutheria, Pi	Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo.	ini; Homir	idae; Homo.
RENCE	1 (bases 1 to 1444)	to 1444)			
THORS	Andersson, B.	, Wentland,	4.A., Ricafrente	J.J.Y., Liu	Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A.
TLE	A 'double ac	laptor, metho	od for improved	shotqun 11	A 'double adaptor' method for improved shotqun library construction
URNAL	Anal. Bioche	em. 236 (1),	Anal. Biochem. 236 (1), 107-113 (1996)	•	•
DLINE	96207227				
RENCE	2 (bases 1 to 1444)	to 1444)			
THORS	Yu, W., Ander	sson, B., Wor	Yu, W., Andersson, B., Worley, K.C., Muzny, D.M., Ding, Y., Liu, W.,	',D.M., Dir	19, Y., Liu, W.,
	Ricafrente,	J.Y., Wentlan	Ricafrente, J.Y., Wentland, M.A., Lennon, G. and Gibbs, R.A.	G. and Gik	bs.R.A.
TLE	Large Scale	Concatenation	Large Scale Concatenation cDNA Sequencing	DG.	
URNAL	Unpublished		•	,	
RENCE	3 (bases 1 to 1444)	to 1444)			

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Taluss 1 to 2206)
Barila.D., Plateroti,M., Nobili,F., Muda,A.O., Xie,Y., Morimoto,T. and Perozzi,G.
The Dri 42 gene, whose expression is up-regulated during epithelia differentiation, encodes a novel endoplasmic reticulum resident
                                                                                                         945 TTCACTTGGCGAGGAGCCCGCCTGCTCCGGCCCCTCCTGCAGTTCACCTTGATGATGATG 1004
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Vertebrata, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-SEP-1996) G. Perozzi, Istituto Nazionale Della
Nutrizione, Unit Of Experimental Nutrition, Via Ardeatina 546,
00178 Roma, ITALY
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   ttcacttggcgaggagccgc-tgttccggccctcctgcagttcaccttgatcatgatg
                                                                                                                                                                                                                                bp RNA ROD TOTAL FOR ER transmembrane protein.
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J. Biol. Chem. 271 (47), 29928-29936 (1996)
97094703
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/dev_stage="adult"
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/db_xref-"PID:g1110276"
/db_xref-"PID:g1110276"
/translation="MQNYKYDKAIVPESKNGGSPALNNNPRRSGSKRVLLICIDLECL
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VCNPPFSQINCSEGYIQNYRCRGDDSKVQEARKSFFSGHASFSMYTMLYLVLYLQARF
                                  Genetics, Baylor
Houston, TX 77030, USA
                                                                                                                                     /dev_stage="infant"
/tissue_type="brain"
//clone_lib="Soares library lNIB from IMAGE consortium"
375...1071
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Yu,W. and Gibbs,R.A.
Direct Submission
Submitted M(22-NOV-1995) Molecular and Human
College of Medicine, One Baylor Plaza S930,
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                                                                                                                                                                                                                                                                                                                                                                Score 1131; DB 78;
Pred. No. 0.00e+00;
0; Mismatches 0;
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                                                                                      /organism="Homo sapiens"
/clone="23748"
                                                            Location/Qualifiers
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                                                                                                                        /sex-"female"
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Best Local Similarity 99.9%;
Matches 1137; Conservative
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Phosphatidic acid phosphatase; 35-kDa
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/tissue_type="kidney"
287.1138
/evidence=experimental
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FTRRGARLLRPLLLGFTLLMARYTGLSRVSDYKHHPSDVLAGFAQGALVACCIVFFVS
DLFYTKTTLSLPAPAIRRELLSPVDIMDRSNHHNNV*
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                                                                                                                                                                                                                                                             cctgaaagtcagcgagactataaacgacgcgtgctctgtgcggtggggatcgtcatcg
                                                                                                                                                                                                                                                                               520 CACTGAAAACTGGTGAGAAAAAAAAGACGCTGTGCTCTGTGCCGTGGGGATCGTCATTG
                                                                                                                                                                                                                                                                                                      ccatcctgcggatcatcacgggggaattctaccggatctattacctcaaggaggagtccc
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9
                                                            Length 2206;
                                                                              0; Mismatches 131; Indels
                                                           Score 784; DB 91;
Pred. No. 0.00e+00;
                                                          57.6%; (larity 87.4%; Conservative
                                                                    Local Similarity
                              503
                                                                              951;
                                                           Query Match
                             BASE COUNT
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Direct Submission

Direct Submission

Submitted (10-APR-1996) to the DDBJ/EMBL/GenBank databases. Hideo Kanoh, Sapporo Medical University School of Medicine, Department of Blochemistry: West-17, South-1, Sapporo, Hokkaido 060, Japan (E-mail:kanoh@serpent.cc.sapmed.ac.jp, Tel:011-611-2111(ax.2290), Fax:011-612-5861)

E 2 (bases 1 to 1212)

S Kai,M., Wada,I., Imai,S., Sakane,F. and Kanoh,H.
Identification and CONA cloning of 35-KDa phosphatidic acid phosphatase (type 2) bound to plasma membranes. Polymerase chain reaction amplification of mouse H202-inducible hic53 clone yielded the CDNA encoding phosphatidic acid phosphatase

L J. Biol. Chem. 271 (31), 18931-18938 (1996) /codon_start=1
/product="Phosphatidic acid phosphatase"
/product="Phosphatidic acid phosphatase"
/db_xref="PID191487873"
/translation="MFDKTRLPYVALDVICVLLAGLPFAILTSRHTPFORGIFCNDDS
IKYPYREDITPYALLGGIVTPFOITWAGGESLSVYFNVHANSPYGNPYIATIKAV
REGRISPTSGASSSSTYTDIAKYTIGSLRPHFLATCNPDWSKINCSDGYTEDYICOGREEN
KEGRISPTSGHSSFSMYCMLFVALVLQARWKGDWARLLRPMIQFGILAFSIYVGLSRV ĕ SDYKHHWSDVTVGLIQGAAMAILVALYVSDFFKDTHSYKERKEEDPHTTLHETASSRN 03-OCT-1996 Phosphatidic acid ô 1137 CCACCTCCTGAGCTGTTTTTGTAAATGACTGCT-GACAGCAAGTTCTTGCTGCTCTCCA 1295 1296 ATCTCATCAGACAGTAGAATGTAGGGAAAAACTTTT-GCCCGACTGATTTTTAAAAAAA 1354 Murinae: 620 agicagiccitgactgacatcgctaagiatactataggcagittgcggccgcacticttg 679 711 AGCCAGICITICACAGACAIIGCCAAAGIGICCAIAGGGCGCCIGCGICCICACIICIIG 770 680 gctatctgtaacccagactggtcaaaaatcaactgcagtgatggctatattgaggactac 739 Gaps gg.cctccagagcactttctctgaagcgactgcttgacagcatgtccctgctgctctcca atctcatcagacagtagaatgtagggaaaagctttttgcccgattggattttgaaaacat Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Butheria; Rodentia; Sciurognathi; Muridae; M acid ö Length 1212; phosphatidic Indels for ROD MRNA 1 0; Mismatches 159; Score 102; DB 85; Pred. No. 1.50e-56; 1212 bp mRNA Musculus domesticus kidney

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                                                                                                                    1053 AGTGATGTTCTGGCAGGAT 1071
                                                                                    935 tccgatgtgctggcaggat 953
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larity 67.8%;
Conservative
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a 367 c
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/translation="MDTNKRILCRVGLDVLILLCAGFPILLFFLLGEPYRRGFFCDDE
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LPDWMIECYKKIGIYAFGAVLSQLTTDIAKYSIGRLRPHFIAVCQPQMADGSTCDDAI
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IZRHLLGFINWAWIALSRYSPKKHHWSDVLAGSLIGSISALVVANYYSDLFXRRNT
KPYLGRIYODMNASPAQAIITITN"
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Direct Submission
Submitted (10-0CT-1966) Molecular Cell Biology, University College,
Gower, London WCIE 65F, England
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acid phosphatase type 2"
/codon_start-1
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                                                                                                                                                                 951 TGGCGAGGAGCCCCCCTCCTGCAGTTCACCTTGATCATGATGGCCTTC 1010
                                                                                                                                                                                                                      1071 TITGCICAAGGAGCCCTGGTGCCTGCTGCTAGTTTTCTTCGTGTCTGACCTCTTCAAG 1130
740 atatgtcaagggaatgaagagaaagtcaaggaggaggtgttgttttttactcggggacac 799
                                                                                              891 GCCTCCTTCTCCATGTACACTATGCTGTATTTGGTGCTATACCTGCAGGCCCCCTTCACT 950
                                                                                                                                860 gagactgggcaagactcttacgacccatgctccatttgggctcattgcttttccata 919
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1 (bases 1 to 1622)
2 Abang, M., Zhang, J., Purcell, K.J., Cheng, Y. and Howard, K. The Drosophila protein Wunen repels migrating germ cells Nature 385 (6611), 64-67 (1997)
                                                                                                                                                                                                                                                                                                                                                                      07-FEB-1997
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                                831 AGATGCAGAGGTGATGACAGCAAAGTCCAGGAAGCCAGGAAGTCCTTCTTCTTGGCCAT
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Pred. No. 8.36e-43;
0; Mismatches 57; Indels
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Drosophila melanogaster Wunen gene, complete cds.
173822
1769524
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/map-"45D"
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Drosophila melanogaster
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Best Local Similarity 71.4%;
Matches 142; Conservative
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/product="hydrogen peroxide-inducible protein"
/db_xref="PlD:g1161100"
/db_xre
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Egawa,K., Yoshiwara,M., Shibanuma,M. and Nose,K.
ISolation of a novel ras-recision gene that is induced by hydrogen peroxide from a mouse osteoblastic cell line, MC3T3-El
96032549
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Mus musculus (clone HIC-53) hydrogen peroxide-inducible protein
                                                                              711 AGCCAGICITICACAGACATIGCCAAAGIGICCATAGGGCGCCIGCGICCTCACTICIIG 770
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875 tteateatggtggeetggtaeacagecetaagtegegtateggaetaeaageaceaetgg 934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrogen peroxide; hydrogen peroxide-inducible protein.
Wus musculus (clone: HIC-53) embryo calvariagag cDNA to mRNA.
Mus musculus
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Pred. No. 8.69e-32;
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/dev_stage="embryo"
/tissue_type="calvariagag"
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/organism="Mus musculus"
/clone="HIC-53"
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                                                                                                                                                                                                                                                                                                                            Tobases 1 to 215)
Bennett.A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                              65 nynyggnnvgaakthyythtnvsgadsktvtdsynasgtsssnggt-dgnrsgadsygss 123
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  30-0CT-1996
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Bennett.A., Labaritch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their icontrol fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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Pred. No. 1.12e-04;
84; Mismatches 94; Indels
                                                                                                                                                                                                                                                          Score 35; DB 57; Length 215; Pred. No. 6.42e-06;
                                                                                                                                                                                                                        141 others
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Best Local Similarity 10.5%;
Matches 21; Conservative
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Local Similarity 13.5%;
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//translation-"SLITCWLLPTTAHYTLKSSPPOVVEGENVILSADNLPENITAFA
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(Modeljav.Y., Lucas, R., Barnert, S., von Kleist, S., Thompson, J.A. and Zimmermann, W.A. actionembryonic antigen gene family in the Identification of a carcinoembryonic antigen gene family in the rat: Analysis of the N-terminal domains reveals immunoglobulin-like, hypervariable regions J. Biol. Chem. 264, 6906-6912 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Draft entry and computer-readable sequence [1] kindly submitted by W.Zimmermann 12-JAN-1989.
Location/Qualifiers
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                           206 GGCCAGGAGGCGACCCGGGCGCTGGGTGTGGCGGGACGTTT-CGCGG 264
126 amtsrnrtgktannavdsrnmgdasvgsdkntkkhaknsadgkvgsknngdrnnrygtgt 185
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Rat carcinoembryonic antigen (CEA3) gene, exon X.
M60025_J04626 M22228
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Human prot-oncogene (BMI-1) mRNA, complete cds.
g291872
                                                                                                                                                                                                                                                                                                                      carcinoembryonic antigen.
Rat (strain BD II) liver DNA, clone rnCGM3.
Rattus norvegicus
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Pred. No. 9.77e-02;
0; Mismatches 14;
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138..203
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/gene="CEA3"
729..1088
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Draft entry and sequence in computer readable form for [1] kindly provided by W.R.Jelinek, 28-JUL-1986.

The 4.5S RNA has a short half-life and appears to be associated with poly-A mixes in vivo. It is not a ribosomal RNA. There are approximately 850 copies of the 4.5S RNA gene per haploid mouse entribroleukemia cell genome. The DNA fragment presented here is a monomer unit of a tandem repeating array. The sequence contains an unusually high number of short tandem repeats (positions 75-119,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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1 (bases 1 to 4251)
Schoeniger,L.O. and Jelinek,W.R.
4.55 RNA is encoded by hundreds of tandemly linked genes, h short half-life, and is hydrogen bonded in vivo to poly(A) terminated RNAs in the cytoplasm of cultured mouse cells MO1. Cell. Biol. 6, 1508-1519 (1986)
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Pred. No. 3.50e-01;
0; Mismatches 15; Indels
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                                     'note="nucleolin mRNA and introns"
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Mouse DNA.
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/note="intron 10"
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/note-"intron 6
2068..2191
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/note="intron 7
2700..2854
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/note="intron
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Mouse 4.5S RNA gene.
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Local Similarity 73.7%;
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//translation="MHRTTRIXITELNPHLMCVLCGGYFIDATTIIECLHSFCRTCIV
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KRYLRCPAAMTVMHLRKFLRSKMDIPNTFQIDVMYEEBPLKDYYTLMDIAYIYTWRN
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TPVQSPHPQFPHISSTMNGTSNSPSGNHQSSFANRPRKSSVNGSSATSSG"
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Bourbon, H.-M.M. and Amalric, F.
Nucleolin gene organization in rodents: Highly conserved sequences within three of the 13 introns
Gene 88, 187-196 (1990)
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
                                Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 3203) Alkema, M.J., Wiegant, J., Raap, A.K., Berns, A. and van Lohuizen, M. Characterization and chromosomal localization of the human
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Hum. Mol. Genet. 2 (10), 1597-1603 (1993)
94093545
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Pred. No. 3.50e-01;
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/cell_line="k562"
/germline
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Homo sapiens cDNA to mRNA.
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/note="putative"
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Best Local Similarity 72.1%;
Matches 44; Conservative
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Gaps

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1322 AAAAACTTTTGCCCGACTGATTTTTAAAAAAAAAAAAA 1361

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Direct Submission
Submitted (26-NOV-1996) Nematode Sequencing Project, Sanger Centre,
Blanton. Cambridge CB10 1RO, England and Department of Genetics,
Rashington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
Order of segments is not known: 800 n's separate segments.
Cosmid=12759; Contig ID=00009; Length=35474; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CET27E9 38118 bp DNA HTG 27-NOV-1996
*** SEQUENCING IN PROGRESS *** Caenorhabditis elegans cosmid T27E9;
870-950, 971-1011, 1148-1178, 1698-1767, 1803-1870, 2178-2242, 3081-3136, 3187-3277, 3562-3401 and 3765-3807) some of which are composed almost exclusively of either purines or pyrimidine saymmetrically distributed to one DNA strand. Others contain alternating purines and pyrimidines. The biological significance of these short tandem repeats is unknown.
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* the sequence data presented in this record will be replaced

*by a single fainished sequence with the same accession number.

Location/Qualifiers
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Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditidae;
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Cosmid=T27E9; Contig ID=00598; Length=2467; Order=Unknown;
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1 bp upstream of EcoRI site; chromosome 6 (tentative).
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Pred. No. 1.22e+00;
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1364..1458
/note="4.55 RNA"
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Caenorhabditis elegans.
Caenorhabditis elegans
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Best Local Similarity 65.1%;
Matches 56; Conservative
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Best Local Similarity 82.5%;
Matches 33; Conservative
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jes@sanger.ac.uk or iw@nematode.wustl.edu
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments.
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                                                                    Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone T28AB; HTGS phase 1.
                                                                                                                                                                          91877160
HTG: HTGS-PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
Elekaryotes: Metazoa; Nematoda;
Secernentea: Rhabditia; Rhabditida: Rhabditina; Rhabditida; Rhabditida: Rhabditida; Rhabditida: Rhabditida; Rhabditida: Rhabditida; Rhabditi
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* the sequence data presented in this record will be replaced
*by a single finished sequence with the same accession number.
                                09-MAR-1997
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Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CBIO
1RQ, UK and Department of Genetics, Washington University, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-NOV-1996) Nematode Sequencing Project, Sanger
Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *** WARNING: Phase 1 High Throughout Genome Sequence ***
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09-MAR-1997 (Rel. 51, Last updated, Version 1)
Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
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/clone="T28A8"
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Pred. No. 1.22e+00;
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nes 33; Conservative
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HTG; HTGS_PHASE1
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Z92813;
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AUTHORS
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                                                                                                                                                                                                                                                           SOURCE
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Submitted (11.MAR-1997) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Mashington University, St. Louis, Mo 63110, USA. E-mail: jes6sanger.ac.uk or rw@nematode.wustl.edu IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Nork on the sequence is in progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEY76A2 170789 bp DNA HTG 12-MAR-1997
Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from
292866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG: HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryotae: mitochondrial eukaryotes; Metazoa; Nematoda;
Secernetrea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * This sequence is unfinished. When sequencing is complete, the sequence data presented in this record will be replaced *by a single finished sequence with the same accession number.
                                                        IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Mork on the sequence is in progress and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                          /chromosome="III"
Sequence 58382 BP; 18078 A; 10005 C; 10370 G; 17347 T; 2582 other;
                                                                                                                                the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *** WARNING: Phase 1 High Throughout Genome Sequence ***
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 58382;
                                                                                                                                                                                                   with foreign sequence from E.coli, yeast, vector, phage et.
Order of segments is not known; 800 n's separate segments.
Key
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51677 a 28129 c 29296 g 48657 t 13030 others
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.9%; Score 26; DB 5; Length 5836
Best Local Similarity 82.5%; Pred. No. 1.22e+00;
Matches 33; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 53626 aaaaatttgttaccgaatgttttttgaaaaaaaaaaa 53665
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/clone="Y76A2"
                                                                                                                                                                                                                                                                                                  1..58382
/organism="Caenorhabditis elegans'
/clone="T28A8"
Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or
rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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Gaps

Score 26; DB 110; Length 170789; Pred. No. 1.22e+00; 0; Mismatches 7; Indels 0;

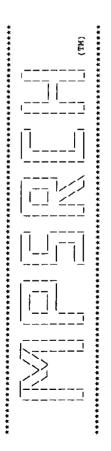
Ouery Match Best Local Similarity 82,5%; Matches 33; Conservative

BASE COUNT ORIGIN

Db 16617 aaaaatttgttaccgaatgttttttgaaaaaaaaaaa 16656

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6 11:57:17 1997 Search completed: Thu Nov Job time: 1277 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Tue Nov 4 10:25:03 1997; MasPar time 8.34 Seconds 791.390 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

>US-08-842-827-6 (1-311) from US08842827.pep 2326 I MONTKYDKAIVPESKNGGSP......RKEILSPVDIIDRNNHHNMM 311 Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Mean 47.573; Variance 83.956; scale 0.567 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	.55e-66	.43e-04	.91e-04	.91e-04	.63e-03	.63e-03	4.72e-03	.31e-02	.42e-01	1.76e-01	.31e-01	.76e-01	.76e-01	.15e-01	.15e-01	.15e-01	.15e-01	.52e-01	.15e-01	.52e-01	.35e-01	.13e+00
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Description	HYPOTHETICAL 39.0 KD	POSSIBLE GUSTATORY RE	PROBABLE CALCIUM-TRAN	HYPOTHETICAL 27.6 KD	PROBABLE G PROTEIN-CO	PROBABLE G PROTEIN-CO	NADH-UBIQUINONE OXIDO	HYPOTHETICAL 46.4 KD	U25 PROTEIN.	HYPOTHETICAL 37.4 KD	YOP PROTEINS TRANSLOC	LATENT MEMBRANE PROTE	POTASSIUM CHANNEL PRO	HYPOTHETICAL 23.7 KD	SRG-3 PROTEIN.	LATENT MEMBRANE PROTE	LATENT MEMBRANE PROTE	SODIUM- AND CHLORIDE-	HYPOTHETICAL 287.5 KD	GENOME POLYPROTEIN.	TYPE 4 PREPILIN-LIKE	LENS FIBER MAJOR INTR
ដ	YSX3_CAEEL	GU01_RAT	ATC5_YEAST	YG1P_YEAST	EDGL_MOUSE	H218_RAT	NU4M_CAEEL	YBAR_BACSU	VU25_HSV7J	YIC3_YEAST	YSCU_YERPS	LMP1_EBVC	CIK6_HUMAN	YAC1_LEGPN	SRG3_CAEEL	LMP1_EBV	LMP1_EBVR	NTBE_CANFA	YBA4_YEAST	POLG_BVDVS	LEP3_VIBCH	MIP_RANPI
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Length	341	185	1571	239	180	352	409	434	320	346	354	404	529	208	332	386	386	614	2493	3898	253	263
å Query Match	18.5	5.2	5.2	5.1	4.8	4.8	4.8	4.4	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1
Score	431	122	120	118	111	111	112	103	100	101	6 6	101	101	97	97	97	97	86	97	96	96	92
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87 tvlfveyyrmqkvesninnpryrwrnnhlhvlfvrlltyfgysqigfvmnialnivtkhv 146

28 islfifflataavtvivptllgvsqrgffcdddsiryeyrk-dtitavglmlynlvlnaa 86

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383 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	TET	18.5%; arity 31.7%; Conservative
4444444444444	DE STAND 96 (REL. 34 96 (REL. 34 96 (REL. 34 CAL 39.0 KD DITIS ELEGA.) METAZOA; FROM N.A. ISTOL N2; TSTOL	Similarity 83; Conse
00000000000000000000000000000000000000	YSX3_CAEEL STANDAR 010022; 01-0CT-1996 (REL. 34, 01-0CT-1996 (REL. 34, 01-0CT-10CT-1996) (REL. 34, 01-0CT-10CT-1996) (REL. 34, 01-0CT-10CT-1996) (REL. 34, 01-0CT-10CT-1996) (REL. 34, 01-0CT-10CT-1996) (REL. 34, 01-0CT-1996) (REL. 34, 01-0C	Match Local Sin Hes 83;
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MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH C., PEPETEL F., SERIL P., SCHRAMM S., SHOGREN T., SMITH V., TAYLOR P., WEI Y., WEI Y., BOTSTEIN D., DAVIS R.W.; SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIEGER M., MUELLER-AUER S., BRUECKNER M., SCHAEFER M.;
SUBMITTED (14AY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
EMBL; 272821; E243385; -.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
                                                                                                                    SEQUENCE OF 1-222 FROM N.A. MULLIDAM CO. YEAL P., KOMP C., MULLIDAN J.T., DIEFRICH F.S., HENNESSEY K.M., SEHL P., KOMP C., WELLY T. ATALOR P., NAKAHARA K., ROBERTS D., DAVIS R.W.; SUBMITTED (FEB-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- CATALVITIC ACTIVITY: APP + H(2)0 = ADP + ORTHOPHOSPHATE.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILMARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST NNOTATION UPDATE)
HYPOTHETICAL 27, 6 KD PROTEIN IN RELIGES ACRI INTERGENIC REGION.
                                                                                                                                                                                                                                                                                        (E1-E2 ATPASES).

EMBL; U18922; G603407; -.

EMBL; U10718; G533146; -.

PIR; S30822; S30822.

PIR; S50041; ATPASE_E1_E2.

HYDROLASE; CALCIUM TRANSPORT; TRANSMEMBRANE; PHOSPHORYLATION; MAGNESIUM; ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 120; DB 1; Length 1571;
Pred. No. 2.91e.04;
29; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 239;
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Pred. No. 5.91e-04;
21; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SACCHARONYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
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POTENTIAL.
POTENTIAL.
7; 671C7F20 CRC32;
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152 PO
185 PO
27649 MW;
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Best Local Similarity 20.0%;
Matches 18; Conservative
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Best Local Similarity 27.4%;
Matches 17; Conservative
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132
165
139 AA;
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P52592;
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P53223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 llvflsilisllvsqlhnsvvlgltyfksvdishffc-dpsllinlacsdtftnnivmyf 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C / AB972;
DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,
AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHERRY D.M.,
CHUNG E., DUNCAN M., GIZMAN E., HARTZELL G., HUNICKE-SMITH S.,
HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FISHER; TISSUE-LINGUAL EPITHELIA;
MEDLIKE; 913813.
ABE V. KUSAKABE Y. TANEMURA K., EMORI Y., ARAI S.;
PEBS LETT. 316:253-256(1993).
- FUNCTION: POSSIBLE TAGER RECEPTOR.
- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
- STRIED SPECIFICITY: TONGUE-SPECIFIC.
- SMILLARIY: TONGUE-SPECIFIC.
PIR: $28996; $28996.
GCRDB: GCR_0825.
                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 122; DB 4; Length 185
Pred. No. 1.43e-04;
30; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00237; G_PROTEIN_RECEPTOR.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).
YER166W OR SYGR-ORF?
                                                                                                                                                                                                          01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
POSSIBLE GUSTATORY RECEPTOR CLONE PTE01 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 vgaisgflpi-sgiffs-yy-kivssilrmpspggkyk 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OEF181BD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1571 AA
                                                                                                                                                                      185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                   PRT;
                    267 vytctfwtdlfsnnstesetgp 288
                                                 268 CCIVFFVSDLFKTKTTLSLPAP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
20605 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (REL. 27, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 28.6%;
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111
422
622
1052
1338
160
1822
71855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 AA;
                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                          RATTUS NORVEGICUS
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 3
ATC5_YEAST
P32660;
                                                                                                                                       RESULT 2
ID GU01_RAT
AC P35894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
TRANSMEM
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SEQUENCE
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SOLUTION

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38734 MW;
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 lse-ilvficiiffip 87
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                     CAENORHABDITIS ELEGANS
                                                                                                                                                            352 AA;
                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
   35
60
67
96
110
129
148
174
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YBAR_BACSU
                                                                                                                                                                                                                                                                               NU4M_CAEEL
            DOMAIN
TRANSMEM
DOMAIN
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TRANSMEM
                                                                                                                                         CARBOHYD
                                                                                                                                                            SEQUENCE
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    FRANSMEM
                                          PRANSMEM
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                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                     -i-SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i-SIMILARIY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL: 120334; G438787; --
G-PROTEIN COUPLED RECEPTOR: TRANSMEMBRANE.
                                                                                              MEDLINE; 94116980.
WILKIE T.M., CHEN Y., GILBERT D.J., MOORE K.J., YU L., SIMON M.I.,
COPELAND N.G., JENKINS N.A.;
GENOMICS 18:175-184(1993).
                                      MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ROĐENTIA.
                                                                                                                                                                                                                                                                                                                                          ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
G
                                                                                                                                                                                                                                                                                                                    Score 111; DB 3; Length 180;
Pred. No. 6.63e-03;
8; Mismatches 19; Indels
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1 LIKE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-BRAIN, AND LUNG;
MEDLINE, 9437312, BROWE C.S., GASKIN A.A., LADO D.C., SHAW MACLENNAN A.J., BROWE C.S., GASKIN A.A., LADO D.C., SHAW MACLENNAN A.J., STOI-209(1994).
                                                                                                                                                                                                                                     4 (POTENTIAL).
EXTRACELIGIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                       130 vlcvvtifsvillaivalyvriyfvvrsshadvagpqtlallktv 174
                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEE-1996 (REL. 33, CREATED)
01-FEE-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROBABLE G PROTEIN-COUPLED RECEPTOR H218 (AGR16).
                                                                                                                                                                                                                                                                                                 MW; C8C3730F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                      352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RAT)
                                                                                                                                                                                                                                                                                      180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          T 6
H218_RAT
P47752;
                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                TRANSMEM
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DOMAIN
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PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 fllftvmfsflifnn-fswgglflvldsysfillivmslfilgiivise-knn--nlli- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BELEATOL NO:
MEDLINE; 92201635.
MEDLINE; 92201635.
OKINGTO R., MACFARLANE J.L., CLARY D.O., WOLSTENHOLME D.R.;
GENETICS 130:471-488(1992).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
EMBL; X54522; G559502; -.
PIR; S26033; S26033.
SEQUENCE 409 Ab; UBIQUINONE; MITOCHONDRION.
SEQUENCE 409 Ab; 47206 MW; DC040448 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
60
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1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST NNOTATION UPDATE)
HYPOTHETICAL 46-4 KD PROTEIN IN RRNG-FEUC INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // Match
Local Similarity 27.6%; Prede, No. 4/72e-03.
Local Similarity 27.6%; Prede, No. 4/72e-03.

Conservative 25; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111; DB 4; Length 352
Pred. No. 6.63e-03;
8; Mismatches 19; Indels
                                                                                                                             4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                      2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 vlcvvtifsvillaivalyvriyfvvrsshadvagpqtlallktv 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALMITATE (BY SIMILARITY)
2F532027 CRC32;
CYTOPLASMIC (POTENTIAL).
                                                                             3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                        7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1992 (REL. 21, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
NADH-UBLQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 AA.
                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HYPOTHETICAL 37.4 KD PROTEIN IN SSM4-MPI1 INTERGENIC REGION.
                                SACCHAROMICES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L25667; G475126; -.
PLASMID; VIRULENCE; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                             37418 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40381 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.38;
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 21.7%;
Matches 26; Conservative
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                                                                                                                                                                                                                    23
90
1120
147
223
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183
207
                                                                                                                                                                                                                              70
100
127
203
253
291
323
346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSCU_YERPS
P40300;
                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ffdk-slyyvssnlqdffl-vglkffypiyelcdfivdfetg-skivehsksfsdmii-y 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 SFSMYIMLYLVLYLQARFTWRGARLLRPLLQFTLIMMARYTGLSRVSDHKHHPSDVLAGF 260
                                 Ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HERPES SIMPLEX VIRUS (TYPE 7 / STRAIN JI) (HHV7).
VIRIDAE: DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Gaps
                                                                                                                                                                                                                                                                                       Gaps
                            LIU H., YASUMOTO K., HACA K., OHASHI Y., YOSHIKAWA H., TAKAHASHI ISUBWITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
1- SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
EMBL; D84213; G1256150; -.
SUBTILIST: BG11562; YBAR.
                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                         97 feg-aswsmyamlagslvilyvlprfttavpsplvallvmtilavtfhvdvrtvgd
                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                              196 FSGHASFSMYIML--YLVL-YLQARFTWRGARLLRPLLQFTLIMMAFYTGLSRVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 103; DB 11; Length 434; Pred. No. 9.31e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.3%; Score 100; DB 10; Length 320;
Best Local Similarity 20.7%; Pred. No. 2.42e-01;
Matches 29; Conservative 42; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                     Mismatches 18;
                                                                                                HYPOTHETICAL PROTEIN; TRANSMEMBRANE; TRANSPORT
                                                                                                                                                                                                                              POTENTIAL.
D5B6B2CD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                    (REL. 34, CREATED)
(REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                               320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIC3_TERST STANDARD, PRI; 346 AA 01-5584.195 (REL. 31, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                        46435 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 rden-invcfil-ksspykt 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AQGALVACCIVFFVSDLFKT 280
                                                                                                                                                                                                                                                              4.48;
                                                                                                                                                                                                                                                                       Local Similarity 37.5%;
les 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                        434 AA:
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SEQUENCE FROM N.A.
        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          VU25_HSV7J
P52528;
01-OCT-1996 (
01-OCT-1996 (
U25-PROTEIN.
                   STRAIN-168
                                                                                                                       TRANSMEM
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Matches

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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 -clfvl-fvpgl-rkndrasltlsllvsfslgtllgdillhvipeslsgvtdvtmvggai 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 FILIMMAFYTGLSRVSDHKHHPSDVLAGFAGGALVACCIVFFVSDLFKTKTLSLPAPA1 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 vhhnrdhghean-heskqsflilkqesifyslvcflqnhlfvlgprynaivailiiglmp 80
SEQUENCE FROM N.A.
STRAIN-5286C / AB972;
BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
BARRELL B.G., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A.,
GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
CLOIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
WALSH S.V., WHITHEHEAD S.;
SOBMITTED (DEC-1944) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- SNBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
EMBL; 246881; G599976;
EMBL; 247047; G753333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-YPIII;
MEDLINE; 9422840,
BERGHAN T., FRICKSON K., GALXOV E., PERSSON C., WOLF-WATZ
J. BACTERIOL. 176:2619-2626(1994).
-1- FUNCTION: COMPONENT OF THE YOP SECRETION MACHINERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 11;
Pred. No. 1.76e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE7083A8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. AC150C3F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
YOP PROFEINS TRANSLOCATION PROTEIN U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 AA
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POTENTIAL.
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POTENTIAL.
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL PROTEIN; TRANSMEMBRANE, TRANSMEM 3 23 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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TRANSMEM
TRANSMEM
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Matches
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9
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BECKH S., PONGS O.;
EMBO J. 9:1749-1756(1990).

-1- FUNCTION: THIS PROTEIN WEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
ION PERMEABLILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANKEL THROUGH
WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                        BNLF1.
EPSTEIN-BARR VIRUS (STRAIN CAO) (HUMAN HERPESVIRUS 4).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 flaiilliialylqqnw-wtllvdllw-illfmailiwmyyhg-prhtdehhh-ddslp 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 FSMYTMLYLVLYLQARFTWRG-ARLLRPLLQFTLIMM-AFYTGLSRVSDHKHHPSDVLA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       HULF., ZABAROVSKY E.R., CHEN F., CAO S.L., ERNBERG I., KLEIN G., MINBERG G., MINBERG G., J. GEN. VIROL. 72:2399-2409(1991).

-!- FUNCTION: THE LATENT MEMBRANE PROTEIN HAS TRANSFORMING ACTIVITY EMER. X58140; G22938; -.
PIR: JO1434: LABECA.
PIR: 521660; S21660.
                                                                               CNDESIKYPLKTGETIND-AVLCAVGIVIALILALITGEFYR-1YYLKKSRSTIONPY 122
                                                        171 cgiecit-pl-lgqilrqlmvictvgfvvisiadyafeyyqyikelkmskdeikrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 101; DB 6; Length 404; Pred. No. 1.76e-01; 9; Mismatches 23; Indels
Pred. No. 3.31e-01;
13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION; TRANSFORMING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154E84C3 CRC32;
                                                                                                                                                                                                            01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REL. 15, CREATED)
(REL. 15, LAST SEQUENCE UPDATE)
(REL. 19, LAST ANNOTATION UPDATE)
                                                                                                                                                                           404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                       LATENT MEMBRANE PROTEIN 1 (LMP-1) (P63).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTASSIUM CHANNEL PROTEIN KV1.6 (HBK2).
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΨW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.38;
Best Local Similarity 35.1%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 35.000
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43769
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
72
97
1125
1186
404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 92013956.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRADIENT
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                                                                                                                                                      JT 12
LMP1_EBVC
P29362;
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SEQUENCE
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TRANSMEM
TRANSMEM
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                                            -:- THE TAIL. MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLUAR COMPARMENTS.
-:- THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS.
-:- SIMILARITY: BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
EMBL, X17622; G32033; -.
PIR: S15037; S15057.
THE SEGMENT S4 IS PROBABLY THE VOLFAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 mypmtvggkivgs-lcaiagvltialpvpvivsnfnyfyhreteqeeqgqythvtcgqpa 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                      TRANSMEMBRANE; ION TRANSPORT; VOLTAGE-GATED CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 529,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97; DB 10; Ler
Pred. No. 6.15e-01;
12; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Mismatches 46;
                                                                                                                                                                                                                            Y; PHOSPHORYLATION SEGMENT S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 2; 1
Pred. No. 1.76e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| ||:||| :|::|::|| ||::|| ||::|| ||::|| 58 TIKPYHRGFYCNDESIKYPLKTGETINDAVLCAVGIVIAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 pdlratdnglgkpdfpeanrer-rpsylptphrayae 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AA; 23714 MW; CEICOAB4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                           (PROBABLE).
356774CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29, CREATED)
29, LAST SEQUENCE UPDATE)
29, LAST ANNOTATION UPDATE)
KD PROTEIN IN ACN 5'REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REL. 32, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 AA
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                                                                                                                                                                                                                                                                  SEGMENT S2.
SEGMENT S3.
SEGMENT S4.
SEGMENT S5.
SEGMENT S5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 93374864.
MEDLINE; 93374864.
MEDLINE; 93374864.
J. BACTERIOL; 175:566-5676(1993).
EMBL; L22081; G348944; ---
PIR; A48642; A48642.
HYPOTHERICAL PROTHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI;
                                                                                                                                                                                                                            MULTIGENE FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                               58728 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%;
Similarity 34.1%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        larity 20.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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01-NOV-1995 (REL. 32, L
01-CT-1996 (REL. 34, L
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SRG-3 OR CIBFIO.6.
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P46572;
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P37033;
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Query Match 4.2%; Score 97; DB 9; Length 332;
Best Local Similarity 29.6%; Pred. No. 6.15e-01;
Matches 32; Conservative 27; Mismatches 38; Indels 11; Gaps 10;
CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
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Search completed: Tue Nov 4 10:25:51 1997 Job time: 48 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

MasPar time 1029.95 Seconds 1313.733 Million cell updates/sec Thu Nov 6 12:23:32 1997; Run on:

Tabular output not generated.

>US-08-842-827-7 (1-1232) from US08842827.seq 1232 Title:

Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch

362067 segs, 549138275 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC

genbank99

9-1021373 19: BCT 1 25: BCT 2 26: BCT 2 27: BCT 2 28: BCT 3 31: GEN 3 31: GEN 3 32: HTG 1 33: HTG 2 34: HTG 3 35: INV 1 30: GEN 2 38: INV 4 39: INV 5 40: INV 1 46: MAM1 47: MAM2 48: MAM3 49: VRT 1 50: VRT 2 52: VRT 4 53: RAT 1 54: RAT 2 55: RAT 5 6: RAT 4 77: RAT 5 8: PRG 59: PRI 1 60: PLN 5 6: PRI 5 55: RAT 3 6: RAT 4 77: PRI 5 8: PRG 59: PRIN 60: PLN 6 6: PLN 1 69: PLN 1 70: PRI 1 71: PRI 2 72: PRI 3 73: PRI 4 75: PRI 5 75: PRI 6 55: PRI 7 7: PRI 8 8: PRI 7 7: PRI 8 7: PRI 7 7: PRI 8 7: PRI 8 7: PRI 8 7: PRI 8 6: PRI 9 7: PRI 8 7: PRI 9 8: PRI 9 7: PRI 9 8: Database:

Database:

genbank-new3 106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:VRT 114:PHG 115:PLN 116:PR11 117:PR12 118:R0D 119:SYN 120:UNA 121:VRL u-embl50_99

Mean 11.574; Variance 6.325; scale 1.830 Statistics:

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No	Musculus 1.26e-66 mRNA for 7.79e-61	3/48 mKN 1.54e- (clone H 2.95e-	Jast 8.42e-	ten 3.03e-	1.58e-	rote 4.94e- Thor 4 94e-	c 11 4.94e-	312,	DNA sequence fr 4.94e-0	quence ** 4.94e-0	K gene. 4.94e-0	SITEUKIN- 1.316+0	mRNA for 1.51e+0	WA for no 1.51e+0	nRNA for 1.51e+0	for myro 1.5le+0	chromoso 1.51e+0	nence fr 1.51e+0	quence ** 1.51e+0	some 16p1 1.51e+0	osome 16pl 1.5le+	some 16pl 1.51e+0	llax 57kD 4.51e+0	mRNA for 4.51e+00	gene, com 4.51e+0	nid cG1160 f 4.51e+0) * D*	16p1	16p1	* eo	* *	16pl 4.5le+0			03-OCT-1996 for Phosphatidic acid			atidic acid		a. Chordata.	Σ			Bank databases. Hideo Medicine, Department	, Hokkaido 060, Japan Tel:011-611-2111(ex.2290)
Description	House mouse; R.norvegicus	Mus musculus	Drosophila me	Sequence 5 fr	Human CO-029.	Mannose-bindi	Rat PFK-L mRNA for	Human cosmid	Human DNA sec	Human DNA seq	H.sapiens PEX	A.thaliana mRNA for p 1	R.norvegicus	H.sapiens mRN	S. tuberosum m	B.napus mRNA	Homo saptens	Human DNA sec	Human DNA sec	Human chromos	Human chromo	Human chromos	Oxytricha fal	R.norvegicus mRNA for 4	Human Stat2 9	Human cosmid	Human DNA sec		Human chromosome	DNA S	AND C	human bwa sequer Human chromosome			ROD cus kidnev mRNA	7		35-kDa phosphatidic	4 8	elikarvotes: Metazoa:	Sciur			DDBJ/EMBL/GenBank ity School of Medi	, Sapporo, Hok) 1.ac.jp, Tel:01
QI	76	n n.		128278					HSF77D12	HS426N21	HSPEX	ATP22A	RN17BHD1	HSGLUCAR	STBIMPP	BNMYBIPRO	HUM7501	HS106120B	HS440021	HSU91325	HSU91325	HSU91322	OFU89259	RNRPA2 HSTINGGENE	HSU18671	HSCG1160	HS65B7	HSU91327	HSU91323	HS473B4	HS431A14	HSU91321	ALIGNMENTS		mRNA domesti	cds.		acid phosphatase;	CDNA to mRNA	_	OU.	_		996) to the	listry; West-17, South-1, Sapporo, :kanoh@serpent.cc.sapmed.ac.jp, Te -612-5061,
DB	91	98 9	40	57	80	2 5	91	116	74	34	9,	4 1U	16	40	8 8	09	ر د د	20	34	9 ;	116	9	8	117	77	73	34	116	οvo	34	122	6 9			1212 bp Musculus	complet		id pj	kidnev	1000	Eutheria;	1212)	ü	PR-1	est.
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Query Match	10.3	. 4 0 80	e .	2.7	2.4	2.0	2.3	6 6	, c	2.3	64 c	7 7	5.5	2.2	7.7	2.5	9 0	7 7	2.2	2.5	2.2	2 2	2.1	2.2	2.1	2.7	2.1	2.1	7 7	2.1	7.7	7.1.7			D84376 House mou	phosphatase	4376	Phosphatidic	phosphatase. Mus musculus		Vertebrata	(bases	Kanon, H. Direct Submission	Submitted Kanoh, Sa	Biochemistry; West-17, (E-mail:kanoh@serpent. Fax:011-612-5061)
Score	127	23	37	9 6	53	282	78	78	7 8	28	1 9	27	27	27	27	27	7.7	27	27	27	7 50	7.7	56	9 9 9 9	56	2.6 2.6	7 6	26	7 7	26	9 6	9 9		п					pho Mus		Ver				o A ⇔ B
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SULT						
CUS	D84376	1212 bp	mRNA	ROD	03-OCT-1996	
FINITION	House mouse;	Musculus	domesticus kidney	mRNA for	House mouse; Musculus domesticus kidney mRNA for Phosphatidic acid	
	phosphatase, complete cds.	complete	cds.			
CESSION	D84376	ı				
ы	g1487872					
TWORDS	Phosphatidic	acid phos	Phosphatidic acid phosphatase; 35-kDa phosphatidic acid	hosphatidi	c acid	
	phosphatase.					
URCE	Mus musculus kidney cDNA to mRNA.	kidney cD	NA to mRNA.			
ORGANISM	Mus musculus					
	Eukaryotae;	mitochondr	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	etazoa; Ch	ordata;	
	Vertebrata;	Eutheria;	Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	nathi; Mur	idae; Murinae;	
	Mus.					
PERENCE	1 (bases 1 to 1212)	to 1212)				
AUTHORS	Kanoh, H.					

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FMAALPFILIETSTIKPVRRGFYCNDESIKVPLKVSETINDAVLCAVGITVIAILRIT
GEFYRIYYLKEKSRSTIONPYAAJKQVGCFLECCAISOSFTDIAKYSIGRLRPHFL
SVCDPDFSQINCSEGYIONIRCRGEDSKVQBARKSFSGHASFSMFTMLXLULYLQAR
FTWRGARLLRPLLGPLLMAMAFYTGLSRVSOYKHHRSDVLAGFAGGALVACCIVFFVS
DLFKTKTTLSLPAPAIREILSPVDIMDRSNHHNMV"
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/translation="MQSYKYDKAIVPESKNGGSPALNNNPRKGGSKRVLLICLDLFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2206)
Barila,D., Plateroti,M., Nobill,F., Muda,A.O., Xie,Y., Morimoto,T.
and Perozzi,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Dri 42 gene, whose expression is up-regulated during epithel differentiation, encodes a novel endoplasmic reticulum resident
                           Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                           681 TOTTGGCCTCCTGCAGGGGGCACTGGTGGCTGCCTCACTGCTACATCTCAGACTT 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-SEP-1996) G. Perozzi, Istituto Nazionale Della Nutrizione, Unit Of Experimental Nutrition, Via Ardeatina 54 00178 Roma, ITALY
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Pred. No. 7.79e-61;
0; Mismatches 177; Indels
                                                                                                                                                                                                                        RNDR142 2206 bp RNA ROCYEGIO. ROCYEGICUS MRNA for ER transmembrane protein.
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/db_xref="PID:e283078"
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J. Biol. Chem. 271 (47), 29928-29936 (1996)
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410..1348
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/dev_stage="adult"
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GAFLEGVSASQSLTDIAKTIGSLRPHELAIUNPDGKINCSDGYIEDVICOGNBEKV
KEGRLSFYSGHSSFWYCMLFALVLOARWKGDWARLLRPWLOFGLIAFSIYVGLSRY
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                                                                                                                                                                                                                                                                                                                   /product="Phosphatidic acid phosphatase"
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                  Kal,M., Wada,I., Imal,S., Sakane,F. and Kanoh,H. Identification and cDNA cloning of 35-KDa phosphatidic acid phosphatase (type 2) bound to plasma membranes. Polymerase chain reaction amplification of mouse H202-inducible hic53 clone yielded the CDNA encoding phosphatidic acid phosphatase 1 biol. Chem. 271 (31), 18931-18938 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggactacatatgicaagggaatgaagagaaagtcaaggagggggggtggtgttttttattc 792
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Pred. No. 1.26e-66;
0; Mismatches 289; Indels
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                                                                                                                                                                                                               /organism-"Mus musculus"
                                                                                                                                                                                                                                 /tissue_type="kidney"
287..1138
/evidence=experimental
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l Similarity 59.8%;
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/db.zere="Pib:g1710276"
/translation="MONYKYDRAIVESKNGGSPALNNNPRRSGSKRVLLICLDLFCL
FMAGLPFLIIETSTIKPYHRGFYCNDESIKYPLKTGETINDAVLCAVGIVIALIALIT
GEFFRIYLIKKSSTIKPYHRGFYCNDGSFLFGCALSGSFFDLAKVSIGRLERPHFLS
VCNPDFSQINGSEGYIQNYRCRGDDSKVQEARKSFFSGHASFSHYTMLYLVLYLQARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotzen mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1444)
Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A. A 'double adaptor' method for improved shotgun library construction 9620727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Genetics, Baylor
S930, Houston, TX 77030, USA
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/tissue_type="brain"
/clone_lib="Soares library INIB from IMAGE consortium"
375,-1076
cgaggagaagacagcaaagtacaggaggccaggaaatccttcttctcgggccacgcctcc 1015
                                                         ttctccatgttcacaatgctgtatctggtgctttatctacaggcccgcttcacctggcgt 1075
                                                                                                                                                                                     ggattgtcacgtgtatctgactacaaacaccatcctagcgatgtcctggcaggatttgcc 1195
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Yu.W., Andersson, B., Worley, K.C., Muzny, D.M., Ding, Y., Liu, W.,
Ricafrente, J.Y., Wentland, M.A., Lennon, G. and Gibbs, R.A.
Large Scale Concatenation cDNA Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaccctacgtggcagcactctataagcaagtgggctgcttcctctttggctgtgccatc 791
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                                                                                                                      gggcccggctcctccgcccctcctgcagttcactttgctcatgatggccttctacacg
                                                                                      514 TITGGGATGIACTGCATGGTGTTCTTGGCGCTGTATGTGCAGGCACGACTCTGTTGGAAG
                                                                                                                                                     574 TGGGCACGGCTGCTGCGACCCACAGTCCAGTTCTTCCTGGTGGCCTTTGCCCTCTACGTG
                                                                                                                                                                                                                  GGCTACACCCGCGTGTCTGATTACAAACACCACTGGAGCGATGTCCTTGTTGGCCTCCTG
                           454 AGGGGAAACCCIGCIGAIGICACCGAGGCIAGITGICITICIACICGGGACACICITIC
                                                                                                                                                                                                                                                 1196 caaggagetetggtggcetgetgeatagtgttettegtgtetgaeetetteaa 1248
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Pred. No. 1.64e-51;
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Submitted (22-NOV-1996) Molecular and
College of Medicine, One Baylor Plaza
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              bp mRNA mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"unknown"
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Yu, W. and Gibbs, R.A.
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Best Local Similarity 61.6%;
Matches 295; Conservative
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Human clone 23748
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/product="hydrogen peroxide-inducible protein"
/db_xref="pin:gil61100"
/db_xref="pin:gil61100"
/translation="ARASLEIARPVCEGTGGRRPTGRDEPALREGAPERQIAASTVVK
ESRRHCSVGRRPIQTGPGPCSRQSKRLAVAMGGRHPEGGALGIGYLDRRGLFLPPLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGDTIQPVTWFDKTRLPYVALDVICVLLAGLPFAILTSRHTPFQRGIFCNDDSIKYPY
REDTIPFALLGGIVIPFCTITWSGESLSVYFWTHJENSRFWDPYTATIKKAVGAFLF
GVGASQSLTDIAKTIGSLRPHFLAICNPDASKINCSDGYIEDVICQGNEEKVKEGRL
SFSGILFILYVLHAVCRTLSSRRLARLLRPMLQFGLIAFSIYVGLFSSV"
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1 (bases 1 to 1490)

Egawa, K., Yoshiwara, M., Shibanuma, M. and Nose, K.

Isolation of a novel ras-recision gene that is induced by hydrogen peroxide from a mouse osteoblastic cell line, MC313-El

FEBS Lett. 372 (1), 74-77 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUSHPIP 1490 bp mRNA ROD 11-JAN-1996
Mus musculus (clone HIC-53) hydrogen peroxide-inducible protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tacacgggactgtctcgcgtatcagaccacaagcaccatcccagtgatgttctggcagga 1150
                                                                                                                                                                                                                                                                                                                                                                                                             agatgcagaggtgatgacagcaaagtccaggaagccaggaagtccttcttctctggccat 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151 tttgctcaaggagccctggtggcctgcttgcatagttttcttcgtgtctgacctcttcaa 1209
                                                   328 AGCCAGTCTCTGACAGACCTGGCCAAGTACATGATTGGGCGTCTGAAGCCCAACTTCCTA 387
                                                                                                                     agigicigoaacccigatitcagccagatcaactgcicigaaggciacattcagaactac 911
                                                                                                                                                                                388 GCGTCTGCGACCCGACTGGAGCCGGGTCAACTGCTCGGTCTATGTGCAGCTGGAGAAG 447
                                                                                                                                                                                                                                                                                                             448 GIGIGCAGGGGAAACCCIGCIGAIGICACCGAGGCCAGGIIGICIIIICIACIICGGGACAC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACGIGGGCTACACCCGCGTGTCTGATTACAAACACCACTGGAGCGATGTCCTTGTTGGC 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA.
agccagtctttcacagacattgccaaagtgtccatagggcgcctgcgtcctcacttcttg
                                                                                                                                                                                                                                                                                                                                                                                  gootcottotocatgtacactatgctgtatttggtgctatacctgcaggcccgcttcact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tggcgaggagcccg-ctgctccggccctcctgcagttcaccttgatcatgatggccttc
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hydrogen peroxide; hydrogen peroxide-inducible protein.
Mus musculus (clone: HIC-53) embryo calvariagag cDNA to
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No. 2.95e-19;
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/cell_type="osteoblast"
/dev_stage="embryo"
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LPDWMIECYKKIGIYAFGAVLSQLTTDIAKYSIGRLRPHFIAVCQPQMADGSTCDDAI NAGKYTQEFTCKGVGSSARMLKEMRLSFPSGHSSFTFFAAVYLLLYLORENTWRGSKL LRHLLQFLFINVAWYTALSRVSDYKHHWSDVLAGSLIGSISALVVANYVSDLFXKPNT RPYLGRTYQDNNASPAQAITITIN" BASE COUNT 469 a 392 c 367 g 383 t 11 others ORIGIN		11	Oy 588 GCGACCCACAGTCCTCCTGGTGGCCTTTGCCCTCTACGTGGGCTACACCGGGT 647 Db 913 atcggactacaagcaccactggtccgatgtgct 945	RESULT 6 LOCUS 128278 215 bp DNA PAT 30-OCT-1996 DEFINITION Sequence 5 from patent US 5569830. ACCESSION 128278 NID q1819054	WORDS RCE RGANISM ERENCE UTHORS ITLE	Ce Location/Quali	Ouery Match Duery Match Best Local Similarity 12.3%; Pred. No. 3.056-05; Matches 26; Conservative 88; Mismatches 96; Indels 2; Gaps 2; Matches 26; Conservative 88; Mismatches 96; Indels 2; Gaps 2; Db 6 masssvvsrtascndkakdgnttsswttdconrupycdtdtyrvnndsgnkyssan 65 :::::::::::::::::::::::::::::::::::
Gaps acttc 41 ACGCT 83	84 84 80 84	OY 144 CGGTCCAGATACCATCACCACGGGTCATGGGTGGGTCACCATCAGGCCACCGTCAT 203 Db 540 cgttatggagtattggagaatctctgtctgtttactttaatgctttgcattcgaattcctt 599	Db 600 tgrcggcaatccctacatagccaccatttacaaagccgtcggagccttttgttcggagt 659 1 1 1 1 1 1 1 1 1	Oy 321 rGCCGTGAGCCAGTCTCTGACAGACCTGGCCAAGTACATGGGCGTCTGAAGCCCAA 380 Db 720 cttcttggctatctgtaaccagactggtcaaaatcaactgcagtgatgatggctatttga 779	780 441 838 501	RESULT 5 LOCUS DMU73822 1622 bp DNA INV 07-FEB-1997 DEFINITION Drosophila melanogaster wunen gene, complete cds. ACCESSION U73822 NID 91769524	AGRDS RCE RGANISM GANISM CTHORS JTHORS JTHORS JTHORS JTHORS JTHORS JUNES SOURCE CDS

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1165 AAAATGTAATGTATATGTGGTTTTTAGTAAAATAGG-GCACCTGTTTCACAAAAAAAAA 1223
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Best Local Similarity 85.0%;
Matches 34; Conservative
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Linnenbach, A.J.

Linnenbach, A.J.

Molecular cloning of CDNA for the human tumor-associated antigen
Molecular cloning of CDNA for the human tumor-associated antigen
CO-029 and identification of related transmembrane antigens
Proc. Natl. Acad. Sci. U.S.A. 84, 6833-6837 (1990)

Draft entry and computer-readable sequence for [1] kindly submitted
AN A.J. Linnenbach, 19-UN-1990, for release after publication.

Author address: A.J. Linnenbach Wistar Institute, Rm 472 3601 Spruce
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEDVGSSSYVAVDILLAVGAIIMILGFLGCGAIKESRCMLLIFFIGLLLILLLQVAT
GILGAVPKSKSDRTVNETILBWYKLLGATGESEKQPORAIIVFQEEFKCCGLVNGAAD
WGNNFQHYPELCACLDKQRPCGSYNGKQVYKETCISFIKDFLAKNLIIVIGISFGLAV
IEILGLYFSWYLYCOIGNR*
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/translation="MAGVSACIKYSMFTFNFLFWLCGILILALAIWVRVSNDSQAIFG
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            Unclassified.

1 (bases 1 to 215)

1 (bases 1 to 215)

Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.

Plant inhibitors of fungal polygalacturonases and their use control fungal disease

Patent: US 5569830-A 5 29-OCT-1996;
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Pred. No. 1.58e-01;
0; Mismatches 16; Indels
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Pred. No. 1.33e-03;
55; Mismatches 56;
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138..851
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Human SW 948 cell line (c
mRNA, clone CO-029-5.
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llarity 12.6%;
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Best Local Similarity 75.0%;
Matches 51; Conservative
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Best Local Similarity
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/product-"mannose-binding protein A precursor"
/db_xref-"PID:g233016"
/tanslation-"MLLDPLPVLLCVVSVSSSGSQTCEDTLKTCSVIACGRDGRDGP
/translation-"MLLDPLPVLLCVVSVSSSGSQTCEDTLKTCSVIACGRDGRDGRDGRDGGLRGLQGPPGKLGPPGSSGPRGGRGGRGGRGGRANKAIEEKLANMEAE
IRLIKSKLQLTHARSMGRKSGKRLFVTNHEKMPFSKVKSLCTELQGTVAIFNRAE
ENRAIQEVATGIAFLGITDEATEGGFWYVTGGRLTYSNWRKDEPNNHGSGEDCVIILD
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/note="Description: mannose-binding protein A precursor,
MBP-A precursor; acute phase reactant; This sequence comes
from Figure 2"
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Wright, C.V.E., Schnegelsberg, P. and De Roberts, E.M.
XIHbox 8: a novel Xenopus homeo protein restricted to a narrow band
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular characterization of the mouse mannose-binding proteins. The mannose-binding protein A but not C is an acute phase reactant J. Immunol. 147 (2), 692-697 (1991)
S42292 943 bp mRNA ROD 16-NOV-1992 mannose-binding protein A precursor-acute phase reactant [mice, Inbred CBA/J, acute phase liver library, pTZ 19 vector, mRNA, 943
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Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenBank staff at the National Library of Medicine created this entry (NCBI globs 42292) from the original journal article. This sequence comes from Figure 2.
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Sastry,K., Zahedi,K., Lelias,J.M., Whitehead,A.S. and
Ezekowitz,R.A.
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Xenopus laevis XlHbox 8 gene for homeodomain protein.
X16849
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Pred. No. 4.94e-01;
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/db_xref="PLD:g58897"
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/db_xre
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LRNEKCHEHYTTEFLYNLYSSEGRGVFDCRTNVLGHLQOGGAPTPFDRNYGTKLGVKA
MLMMSEKLRDVYRKGRVFANAPDSACVIGLRKKVVAFSSVTELKKETDFEHRMPREQW
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EARGRYEELCIVWCVIPATISNNVPGTDFSLGSDTAVNAAMESCDRIKQSASGTKRRV
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all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone; and the assembly was
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Fulton, B. and Rohlfing, T. The sequence of H. sapiens cosmid U54B12
Unpublished (1996)
2 (bases 1 to 38476)
Waterston, R.
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Pred. No. 4.94e-01;
0; Mismatches 10; Indels
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Human cosmid US4B12, complete sequence.
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3 (bases 1 to 38476)
Waterston, R.
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Submitted by:
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-AUG-1994) Laura Gama, 615-343-8258 (lab) 615-343-4539 (fax) e-mail: wrightc@ctrvax.vanderbilt.edu
Data kindly reviewed (22-M) pp De Roberts E.M.
Location/Qualifiers
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Submitted (03-APR-1991) K. Hotta, Second Dept of Internal Medicine,
Submitted (03-APR-1991) K. Hotta, Second Dept of Internal Medicine,
Osaka Diversity Medical School, 1-1-50 Fukushima, Fukushima-ku,
Osaka 553, JAPAN
2 (bases 1 to 2770)
2 (bases 1 to 2770)
Noguchi, T., Nakalima, H., Yamasaki, T., Hamaguchi, T., Kuwajima, M.,
Noguchi, T., Tanaka, T., Kono, N. and Tarui, S.
Rat-liver-type phosphofructokinase mRNA. Structure, tissue
distribution and regulation
Eur. J. Blochem. 202 (2), 293-298 (1991)
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Vertebrata, Eutheria, Rodentia, Sciurognathi; Myomorpha, Muridae,
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Best Local Similarity 79.2%; Pred. No. 4.94e-01;
Matches 38; Conservative 0; Mismatches 10; Indels
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Rat PFK-L mRNA for liver phosphofructokinase.
X58865
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                                                                                                                                                                                                                                                                                        /organism-"Xenopus laevis"
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/tissue_type="liver"
/clone_lib="lambda-gt10"
                                                                                                                                                                                                                                                                                                                                                                        /note="XlHbox 8 protein"
                                                                                                                                                                                                                                                                                                                 /clone_lib="Charon 4A" 70..885
      Development 104, 787-794 (1988)
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/EC_number="2.7.1.11"
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                              revised by [2]
2 (bases 1 to 1584)
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Rattus norvegicus
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/db_xref="PID:g1613888"
/reas1ation="meaptgssvetgkrankgtrialvvevggtlvlgtiletuvsggl
LSt.Qakobyclkpecieaaallskvnlsvdpcdnefreacdgwisnnpipedmpsvg
YppwirhvdlkkikgkpllgfgdtlyreQylfgkt"
21688..21792
 candidate gene product (U60475); end not contained in this
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Eukaryotes; Metazoa; Chordata;
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Eukrebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 38476)
Fulton, B. and Rohlfing, T.
The sequence of H. sapiens cosmid U54B12
2 (bases 1 to 38476)
Waterston, R.
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Human cosmid U54B12; HTGS phase 3, complete sequence.
U73024
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complement(24737..25028)
/rpt_family-"ALU"
25485..25778
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/dote="Grail prediction, score = 81"
/gene="PBX"
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complement(37796..38072)
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/rpt_family="ALU"
31158..31397
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31432..31479
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complement(27663.
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Submitted (01-OCT-1996)
3 (bases 1 to 38476)
Waterston, R.
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Submitted (15-OCT-1996)
Submitted by:
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Best Local Similarity 83,3%;
Matches 35; Conservative
                                                                                                                           /gene="PEX
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REFERENCE
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                                                                                                                                                                                                                                                                                          The orientation of U54B12 is unknown. The start of U54B12 is at base position 1 of this sequence; the end is at base position 38476 of this sequence.
                                                                                                                                         M. Grieff, R. Mazzarella, M.P. Whyte, R.V. Thakker, R. Wilson, S. Chisso, and D. Schlessinger. Y-linked hypophosphatemia candidate gene region: sequence data on 80 kb containing spermine synthase and the 5' region of PEX', in preparation.
                               SOURCE INFORMATION: This clone is from a chromosome X specific cosmid library LLOXNCCOI U. The source of the chromosomes was a human/hamster hybrid, 5M07297-F from Robert Nussbaum at University of Pennsylvania School of Medicine. Vector: Lawrist16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"partial of X-linked hypophosphatemic rickets
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14290..14522
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/rpt_family="ALU"
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Location/Qualifiers
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complement(11315..11605)
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complement(18684..19234)
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confirmed by restriction digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2981..3244)
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4985..5263
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                                                                                                                         Clone reference:
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Department of Genetics, Washington University, St. Louis, MO 63110, USA, and e-mail: saplens@watson.wustl.edu
Genome Sequencing Center
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FICE: This sequence may not be the entire insert of this clone. may be shorter because we only sequence overlapping sections:e, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest

SOURCE INFORMATION: This clone is from a chromosome x specific cosmid library LLOXACCO! 'U'. The source of the chromosomes was a human/hamster hybrid,GM0729'-F from Robert Nussbaum at University of Pennsylvania School of Medicine. Vector: Lawristi6

Clone reference:
M. Grieff, R. Mazzarella, M.P. Whyte, R.V. Thakker, R. Wilson, S. Chissoe, and D. Schlessinger. 'X-linked hypophosphatemia candidate gene region: sequence data on 80 kb containing spermine synthase and the 5' region of PEX', in preparation.

NEIGHBORING SEQUENCE INFORMATION:

The orientation of U54B12 is unknown. The start of U54B12 is at base position 1 of this sequence; the end is at base position 38476 of this sequence.

This clone contains STSs sWXD1735 and sWXD1737 Location/Qualifiers 1.38476 /organism="Homo sapiens" /note="Grail prediction, score = 88" 14290..14522 /note="multiple Est hits, see T63265" complement(16529..16799) /rpt_family="ALU" 17004..17296 /rpt_family="ALU" complement(12648.12939) /rpt_family="ALU" 13729.13827 complement(11315.11605) /rpt_family="ALU" 12258.12540 /clone_lib-"LLOXNCC01-U" /map-"xq22.1-22.2" complement(2981.3244)
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repeat_region

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repeat_region

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/product="partial of X-linked hypophosphatemic rickets candidate gene product (U60475); end not contained in this
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Human DNA sequence from fosm1d F77D12 on chromosome 22q12-qter
contains ESTs, tRNA.
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join(21676..21793,27137..27205,35710..35936)
/gene="PEX"
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Pred. No. 4.94e-01;
0; Mismatches 7
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/rpt_fanily_ALU"
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31432.31479
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Best Local Similarity 83.3%;
Matches 35; Conservative
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22g12-gter.
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KEYWORDS
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	repeat: matches 234302 of
Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo. REFERENCE 1 (bases 1 to 41611)	repeat_region //10.00 repeat: matches 0/104 of consensus repeat_region //10.17293 //note="FLAM_C repeat: matches 1182 of consensus
Hunt, A. Direct Submission	
JOURNAL SUBMITTED (06-NOV-1996) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK, E-mall enquires: humquery@sanger.ac.uk Clone	2 4
COMMENT IMPORTANT: This sequence is the entire insert of clone F77D12. The true left end of clone F77D12 is at 1 in this sequence. The true	/note="Mikz repeat: marches 12351 of consensus repeat_region 118988.19083 // 11888.19083 // repeat_region 7.016988.18081 repeat: matches 35.128 of consensus
, tong 1, by	, ,
F77012 is part of a contig isolated using YESFCTIL TOWNER TIDITARY Centre chromosome 22 XAC contig described in Collins. I.E. et al	/NOCE
377 Suppl., 367-379.	/product="F77b12.t1" repeat_redion 2089021184
source 141611 /organism="Homo sapiens"	
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/note="MIR repeat: matches 32135 o pt complement(join(39214042,4860500	
78508012,1097211089,1274512848,1444614590, 1472514864,1518315321,1631416403,2041520489,	/note="AluSx repeat: matches 302 2576725895
3217032377,3839938510)) /note="match: H55150 N40068 W24192 F13133; match: R13875	
R60279 H07047 T08420; match: H56574 R69765 T75418 match: R13672 H55094 W03454"	/note*"MIR2 repeat: matches 9318 of consensus repeat_region 2611726405
	/note="AluSg repeat: matches 2981 2781728101
	/note="AluSc repeat: matches 2895 of consensus repeat_region 2871629017
64536758 /note="AluSx repeat: matches 3021 c	
302 of	
817 of c	
80678362 /note="Alux repeat: matches 2981 of	
2 of consensus"	μ.
97959917 /note="MIR repeat: matches 20147 of co	/note="match: 5' EST W23521 clone 295490" repeat_region 32709, 33001
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	•
	/note="AluSx repeat: matches 2302 of consensus repeat_region 3523235259
	/note="14 copies of 2 mer 100 % conserved" repeat_region 3571535759
1351113806 /note="AluSx repeat: matches 1297	/note="MER5A repeat: matches 3175 of 3576136057
	0
repeat_region 1421014349 /note="Milk repeat: matches 35190 of consensus" repeat region 16664.16936	/note="MERSA repeat: matches 61165 of consensus repeat_region 3115937450 //arrtial //arrtial
/part	l of
	/note-*MIR repeat: matches 24899 of consensus" repeat_region 3965039942

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Vith foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished sequence: ddd26N21 Contig_LD: 00151 Length: 1888 bp Unfinished sequence: ddd26N21 Contig_LD: 00106 Length: 1888 bp Unfinished sequence: ddd26N21 Contig_LD: 00040 Length: 862 bp Unfinished sequence: ddd26N21 Contig_LD: 02094 Length: 8017 bp Unfinished sequence: ddd26N21 Contig_LD: 02094 Length: 2158 bp Unfinished sequence: ddd26N21 Contig_LD: 02176 Length: 4992 bp Unfinished sequence: ddd26N21 Contig_LD: 02109 Length: 950 bp Unfinished sequence: ddd26N21 Contig_LD: 02099 Length: 950 bp Unfinished sequence: ddd26N21 Contig_LD: 00949 Length: 38703 bp Unfinished sequence: ddd26N21 Contig_LD: 00949 Length: 38703 bp Unfinished sequence: ddd26N21 Contig_LD: 0102 Length: 38703 bp Unfinished sequence: ddd26N21 Contig_LD: 02080 Length: 37705 bp Unfinished sequence: ddd26N21 Contig_LD: 02131 Length: 1244 bp.
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Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton,
Submittedshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated
                   * This sequence is unfinished. When sequencing is complete,

* the sequence data presented in this record will be replaced

*by a single finished sequence with the same accession number.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
426N21; HTGS phase 1.
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[ (bases 1 to 117261)
'note="AluSx repeat: matches 6..297 of consensus"
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                                                                                                                                                                                                                                                                                                               Score 28; DB 74; Length 41611;
Pred. No. 4.94e-01;
0; Mismatches 1; Indels 0
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Best Local Similarity 96.7%;
Matches 29; Conservative
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HTG; HTGS_PHASE1.
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ORIGIN
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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2.3%; Score 28; DB 34; Length 117261;

Query Match

Search completed: Thu Nov 6 12:43:10 1997 Job time: 1178 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Thu Nov 6 12:43:31 1997; MasPar time 132.50 Seconds 970.443 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-842-827-7 (1-1232) from US08842827.seq 1232 Title:

1 ACCATGCAGCGGAGGTGGGT. TGGTACGTCGCCTCCACCCA. Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

142080 seqs, 52183452 bases x 2 Searched:

Dbase 0; Query 0

••

STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq28 lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28

Mean 9.327; Variance 6.638; scale 1.405 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 2 75 6.1 1047 2 010572 Human Natriuretic Pep 1.19e 1.32	Re	Result No.	Score	Query Match	å Query Match Length DB	99	A	Description	Pred. No.
1047 2 010572 Human Natriuretic Pep 2 74 0 123564 Human gene signature 1 91 051746 Oligonucleotide probe 3 1 9 051746 Oligonucleotide probe 3 051746 Oligonucleotide probe 3 04 1 N81164 Base substituted E.co 3 104 1 N81164 Base substituted E.co 3 114 12 070465 Generic DNA sequence 2 114 12 070465 Generic DNA sequence 2 114 12 070469 Generic DN	1	-	83	6.7	1047	7	910572	Human Natriuretic Pep	1.19e-29
74 20 123564 Human gene signature 1 9 9 551746 Oligomucleotide probe 3 204 1 N81164 Base substituted E.co 3 204 1 N81164 Base substituted E.co 3 114 12 Q70467 Generic DNA sequence 2 114 12 Q70469	o	7	75	6.1	1047	~	010572	Human Natriuretic Pep	2.69e-25
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16	17	18	19	50	21	22	23	24	25	26	27	58	53	30	31	32	33	34	35	36	37	38	99	40	41	42	43	44	45
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ALIGNMENTS

010572 standard; DNA; 1047 BP.
010572;
09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
Homo saplens. Domain 23..455 /label- extracellular domain /note- "binds natriuretic peptides A,B and C]" Jubel - cytoplasmic domain / Jubel - cytoplasmic domain / Jubel - cot and prottien kinase activity" wouldfied - site - 24...26 / Jubel - N-glycos_site Location/Qualifiers Domain 456..456 /label- transmembrane domain Domain 479..1047 /label signal sequence Protein 12 /label mature NPBR Peptide RESULT DACKWEED THE STATE STATE

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09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB: AND: BND: CNP: kidney failure; heart failure; protein kinase;
hyperaldosteronism: glaucoma; guanyl cyclase.
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        803 TGTCACTGACGTTGACCCTGGGGGGAGGCTGACCACAACCACTTATGGGATACCCGCACT
                                                                                        gnkmnrycnngdtvntasrmnsngnanknhvssttkdandnngcnnnnrgdvnmkgkgk
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Pred. No. 2.69e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "binds natriuretic peptides A,B and C]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "GC and protien kinase activity"
Modified -site 24..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 C;
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                                                                                                                                                                                                                                                                                                                                                standard; DNA; 1047 BP
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22-JUN-1999, U03586,
23-JUN-1989, US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe
WPI; 91-036711/05.
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Modified -site 35.37
/label= N-glycos_site
Modified -site 161.163
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led -site 244..246
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led -site 277..279
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ied -site 195..1
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d -site 349.3
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ndified -site 600..6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 TGAGCCAGTCTCTGACAGACCTGGCCAAGTACATGAT-TGGGCGGT-CTGAAGCCCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 1047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236; Mismatches 530; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.19e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 G:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.7%; Score 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 0;
22-JUN-1990; U03586.
23-JUN-1989; US-370673.
(GETH ) GENEWTECH INC.
Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
N-PSDB; Q10324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 8.5%;
tes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1047 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             also be prepd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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1143 GATCAGATAGTTGCTGTTFTGTAAAATGTATATGTATATGTGGTTTTTAGTAAAATAGGGC 1202
                                                                                                                                                                                                                                                                                               A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mNA by using polyf'() as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is constructed so as to reflect accurately the relative abundance of different mRRAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 24 A; 7 C; 14 G; 27 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gatcanatagttgctgttttgtaaaatgtaatgtatatntggttttaagtaaaatagggc 60
    human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
                                                                                                                                                                                                                  identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide probe MX14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 20; Length /4;
Pred. No. 1.32e-22;
"...matches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q51746 standard; cDNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-WAY-1993; 108325.
26-WAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.48;
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Local Similarity 95.9%;
Les 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1203 ACCTGTTTCACAAA 1216
                                                                                01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 acctgtttcacaaa 74
                                                                                                                                                                                   Okubo K;
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                                                                                                                                                                                                 WPI; 95-206931/27
                                                                                                                                                             OKUBO K.
                                                         W09514772-A1.
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01-DEC-1993.
                                                                                                                                                                                Matsubara K
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  10;
                                                                                                                                            1190 TAAAAACCACATATACATTTTACAAAACAGCAACTATCTGATCTCTCGGTCCCTT 1131
                                                                                                                                                                                                                                    1070 ATGCTGAGGGCTACCCAGGCATCTCCAGACTCCTGGTCCAGTGCAGGGGCAGGGGCA-GC 1012
                                                                                                                                                                                               160 nnwtaraannyndartddrnhyntnngvnnanngsnnsvnhnvyarnnggnnnathnnra 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 TGACCCGGCTCCAGTCGCGGTCGCAGACGCTAGGAAGTTGGGCT-TCAGACGCCCAATC 350
                                                                                                                   100 gcvynaasvarnashwrnnnntagavasgnsakndhyrtnvrtgnsankngnnvvtnhgh 159
                                                                                                                                                                                                                                                                                                                                                           rnnananrnanntvnvntyrnnnnnnnnnnnnnnnnnnrnnnrarndngvnngnsnmnnagenyd 339
                                                                                                                                                                                                                                                                                                                                                                                                                                   340 gnnnyanvnnntnnnggtrndgnrnvnkmngrryhgvtgnvvmdknndrntdnvnwamgd 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 ndsgdnnnaahysganknnwwtgrnnnwvkgannsdnnncandnddnscdktnnstnanv 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      834 TCAGCCTCGCCCCAGGGTCAACGTCAGTGACAGGCTGGGCTTCCGTTCCAGCTCCTCTT 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774 CITCAGACAGIGCIGIGGGGGICGGGCTITGAAGAAGICIGAGA-IGIAGCAGACAGIGA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                715 GGGCAGCCACCAGTGCCCCCTGCAGGAGGCCAACAAGACATCGCTCCAGTGGTGTT-TG 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trnngacndnnnncnvtnycnrgsnndnnnndsnnndwmnrysnnndnvkgmannhnsnn 639
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    Gaps
                                        wawnrvgnavanavnangrannvdnrnvssnnngacsnynannsavdnknyhdndnnngn 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123564;
02-SEP-1996 (first entry)
Human gene signature HUMGS03416.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
                                                                                                                                                                                                                                                                                                      1011 GGAACCGCTCACTGCTCCCATCAGCCCAGGGTTCCTGGAGCCCGTCCAGAACCCTCA-GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             520 rgssygsomtahgkynnnantghokgovvankhvokkronntrovononkhmrdvooph
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                                                                                                                                                                                                                                                                            220 ngrnvyncgnnnmnhnnnnnanrnnntngdyvnnyndvngnsnragntratgrnwndnrt
                                                                                                                                                                                                                                                                                                                                                                                             952 GCCTAACCAGGCTGGAGGGACCACCTGGGTGGGCATCAGCTGGACTCACAGCAGCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 angtgntnnmngvssnnnnrknmnnknnasmnwrnrwnnnnngnsnryhkgagsrntnsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 TAATCAGACACGCGGGTGT-AGCCCACGTAGAGGCCAAAAGGCCACCAGGAAGAACTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 IGIGGGICGCAGCAGCCGIGCCCACIICCAACAGAGICGIGCCIGCACAIACAGCGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537 GAACACCATGCAGTACATCCCAAAGGAAGAGTGTCCCGAGTAGAAAGACAACCTGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 GGTGACATCAGCAGGGTTTCCCCTGCACCTTC-TCCAGCTGCACATAGACCGAGCAGT
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    10:
    Indels
  Mismatches 575;
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  Conservative 258;
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79;
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1139 CGGTCCCTTCCTTAACCCCATAAAAAGAAGGGGAT 1105
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Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
Disclosure; p; English.

Bischown point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to
the operate a popn of DNR molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                    Gaps
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08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 CCCTGCACACCTTCTCCAGCTGCACATAGACCGAGCAGTTGACCCGGCTCCAG 405
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of 30130nucleotide probe MK14-A consists of nucleotides 5-95 of 302135). It hybridized to all spp. of mycobacterial seted, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                    Oligonuclectide probe MK14-A
Oligonuclectide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 vhsyyvvhvvshhhsvhhvvhhvhhvvhvvhhvhhvhyhvyvsvctcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligo:nucleotide probes specific for Mycobacteria – used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                      795 GCCCAGCCTGTCACTGACGTTGACCCTGGGGCGAGGCTGACCACAACCAC 844
                                                                                                  10 gssvhsyyvvhvvshhhsvhhvvhhvvhhvvhhvhhvhhvhyhvs 59
                                    4; Indels
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Pred. No. 3.66e-08;
2.0%; Pred. No. 3.66e-08;
                                    45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function-multiple cloning site
primer_bind 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
EP-571911-A.
01-DEC-1993;
24-MAY-1993; 108325.
26-MAY-1992; US-689651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-376844/48.
                                                                                                                                                                                                                                                                                                      Q51746 standard; cDNA; 91 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%;
Similarity 9.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1994 (first entry)
                                1; Conservative
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30-MAR-1988, 105163.
03-APR-1987; US-034819.
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Best Local Similarity
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Substitution of supervisors of the supervisors of the supervisors of supervisors 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 thhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnn 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 cynachhddhyvybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 gagcycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydc 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781 GAGCTGGAACGGAAGCCCAGCCTGTCACTGACGTTGACCCTGGGGGGGAGGCTGACCACAA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
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Pred. No. 3.41e-07;
55; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                Length 204;
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                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 1; L
Pred. No. 3.66e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 cncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                           17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 C; 17 G;
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                                                                                                                                                                                                                                                                           47 C;
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larity 8.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 13.3%;
                                                                                                                                                                                                                                                                           21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
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30-MAR-1988; 105163.
03-APR-1987; US-034819.
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                                                                                                                                                                                                                                                                      204 BP;
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EP-285123-A.
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                                                                                                                                                                                                                                                     31-JAN-1994;
                                                                                                          sequence of
                                                                                                                                                                                                                                                                                                Fowlkes DM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or screening a recombinant vector library expressing fusion proteins of screening a recombinant vector library expressing fusion proteins of screening a binding domain and an effector domain or bisclosure; page 35; 255pp; English.

Oldsfolus a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)16(TGC)(NNB)16(TGC)(NNB)16(TGC)(NNB)16(TGC)(NNB)16(TGC)(NNB)16(TGC)(NNB)17. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q10466-68.

Other specified further. Other generic sequences are shown in RS151-54. TSARs are concatenated by these generic sequences are shown in RS151-54. TSARs are concatenated between generic sequences are shown in RS151-54. TSARs are concatenated between proteins or peptides.

CC Committy for a ligand and ascond effector peptide portion that is chantcally or blologically active. They may further comprise a linker peptide between the 2 domains. The oligonicleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues positioned in, or flanking, the unpredicted or variant residues compens. CC compens. Compensing arrangement of conformational rigidity to the peptides. The TSARS compension replace the function of macromolecules, eg. Gelliver a chemically or blologically active molety, eg. metal ion.

CC complex methods of hybridoma formation or in vivo antibody production.

CC The TSARS are easily permedical antibodies and therefore circumvent the need for the compens.
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Generic DNA sequence to generate a random TSAR petide library.
GRAR: totally synthetic affinity reagent; synthetic, binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                            Generic DNA sequence to generate a random TSAR petide library.
TSAR; toctally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     direct and rapid detection in a screening process Sequence 114 BP; 0 A; 2 C; 2 G; 2 T
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                                                                                                                                                                                                                                 can be
                                                                                                                                                                                                                               /note= "this sequence represents '2'; Z
sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36;
                                                                                                                                                       Location/Qualifiers
55..60
                                                                                                                                                                                                                                                                                                                                                  01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UVNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
WPI; 94-279739/34.
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Q70465 standard; DNA; 114 BP.
standard; DNA; 114 BP.
                                        (first entry)
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                                                                                                                                                                                    misc_feature
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18-AUG-1994.
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                                                                                                                                           Synthetic.
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Teachifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or period domain and an effector domain proteins comprising a binding domain and an effector domain proteins of screening a binding domain and an effector domain proteins of screening a binding domain and an effector domain or proteins a generic DAR sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be spinted as follows: K(NNB) G(TGC) (NNB) 11 K(NNB) 14 (TGC) (NNB) 14 K(NNB) G(TGC) (NNB) G(TGC) (NNB) 14 K(NNB) G(TGC) (NNB) 14 K(NNB) G(TGC) (NNB) 14 K(NNB) G(TGC) G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generic DNA sequence to generate a random TSAR-9 petide library.
TARR, totally synthetic affinity reagent; synthetic, binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 2.29e-04;
33; Mismatches 75; Indels
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                                                                                                                                                                                      9 or 12 nucleotides (see
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Location/Qualifiers
55..60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNC-) UNIV NORTH CAROLINA.
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Best Local Similarity 3.6%;
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PT PETENDER, R65152.

Identifying proteins or peptide(s) which bind a ligand - by Identifying proteins or peptide(s) which bind a ligand - by Identifying proteins a recombinant vector library expressing fusion proteins or screening a binding domain and an effector domain proteins by a comperising a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins of 70466 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows:X(NNB)1(TGC)(NNB)4(NNB)4Z(NNB)4Z(NNB)8TGC)(NNB) CC represented as follows:X(NNB)1(TGC)(NNB)4Z(NNB)4Z(NNB)8TGC)(NNB) CC that are not specific peptides generated by these generate sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding commain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also casigned so that the expressed peptide contains are also positioned in, or flanking, the unpredicted or variant residues. These positioned in, or flanking, the unpredicted or variant residues. These crompairs comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active motety, eg. metal contoural or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoms formation or in vivo antibody production.

The TSARs or are easily preserved and therefore circumvent the need for complex methods of hybridoms formation or in vivo antibody production.

The TSARs are easily propried and the forcing activity allowing attention or many and activity and also replace the function of macromolecules, eg. The TSARs are easily the production of macromolecules.
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                                                                                                         30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNLV NORTH CAROLINA.
FOWLKES DM, KAY BK;
                                                                                             US-013416
                                                                                                                                                                                                                               94-279739/34.
WO9418318-A.
18-AUG-1994.
01-FEB-1994; U
                                                                                                                                                                                                                                                                 P-PSDB; R65152
                                                                                      01-FEB-1993;
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ö 0; Gaps Length 114; Score 34; DB 12; Length 114; Pred. No. 2.29e-04; 27; Mismatches 68; Indels Query Match 2.8%; Best Local Similarity 10.4%; Matches 11; Conservative

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63 banbanbanbanbanbanbanbtgcanbanbanbanbanb 108 610 CTGGTGGCCTTTGCCCTCTACGTGGGCTACACCCGCGTGTCTGATT 655 g

Generic DNA sequence to generate a random TSAR peptide library. YARR; totally synthetic affinity resquent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. Q70469 standard; DNA; 114 BP. 07-APR-1995 (first entry) Synthetic. 970469; TRESULT ON THE SOLT ON THE SOL

/*tag= a /note= "this sequence represents '2'; Z can be sequence of 6,9 or 12 nucleotides (see misc_feature comments)" WO9418318-A.

Location/Qualifiers

US-013416. US-176500. US-189331. U00977. 01-FEB-1993; U 30-DEC-1993; U 31-JAN-1994; U (UYNC-) UNIV N 01-FEB-1994; 18-AUG-1994

PROVINCES DN. Kay BK;

PROVINCES DN. Kay BK;

PROPERTY: 94-279739/34.

Identifying proteins or peptide(s) which bind a ligand - by

Identifying proteins or peptide(s) which bind a ligand - by

Identifying proteins or peptide(s) which bind a ligand - by

Identifying a binding domain and an effector domain proteins

PR Screening a recombinant vector library expressing fusion proteins

PR SIGNOBLES PROPERTY OF SEQUENCE OF SECTION OF SECTIO ö 390 CGTCTGCGACCCCGACTGGAGCCGGGTCAACTGCTCGGTCTATGTGCGAGCTGGAGAAGGT 449 3 canbanbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbanban Gaps ö 450 GTGCAGGGGAAACCCTGCTGATGTCACCGAGGCCAGGTTGTCTTCTACT 499 Length 114; Score 34; DB 12; Length 114 Pred. No. 2.29e-04; 31; Mismatches 73; Indels **₹** 4 G; Δ, detection in a screening process. Sequence 114 BP; 0 A; 4 C 2.8%; llarity 5.5%; Conservative 0 A; Local Similarity Seguence Query Match qq ò ò

Generic DNA sequence to generate a random TSAR petide library.
TSAR: totally synthetic affinity rangent: synthetic; binding domain;
effector domain; concatencated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss. /note= "this sequence represents '2'; Z can be sequence of 6, 9 or 12 nucleotides (see comments)" Location/Qualiflers 55..60 Q70468 standard; DNA; 114 BP. 05-APR-1995 (first entry) US-013416. U00977 misc_feature 18-AUG-1994. 01-FEB-1994; 01-FEB-1993; WO9418318-A Synthetic. RESULT

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English. WPI; 94-279739/34. R65154 P-PSDB;

30-DEC-1993; US-176500. 31-JAN-1994; US-189331. (UYNC-) UNIV NORTH CAROLINA.

Kay BK;

Fowlkes DM

comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker

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Synthetic Affinity Reagents peptides. This generate random ISAR (Totally Synthetic Affinity Reagents) peptides. This general formula can also be represented as follows: X(NNB)11(TGC)(NNB) TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specified further. Other generic sequences are shown in Q70466-68. Cother specified further other generic sequences are shown in G8151-54. TSARs are concatenated by these generic sequences are shown in C6151-54. TSARs are concatenated between the sequences are also are larged at least two functional regions - a binding domain with a finity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonuclectides are also designed so that the expressed peptide contains 2 or 4 systeine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compans: comprising a TSAR inding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, thurting domain can be used in vivo to conformation also replace the function of macromolecules, eg. monoclonal or polyclonal artibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody company direct and rapid detection in a screening process.
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ö 606 CTTCCTGGTGGCCTTTGCCCTCTACGTGGGCTACACCCGCGTGTCTGATTACAAACACCA 665 Gaps ö Length 114; Score 34; DB 12; Length 114 Pred. No. 2.29e-04; 33; Mismatches 75; Indels 2.8%; 3.6%; 4; Conservative Query Match Best Local Similarity Matches ò

63 banbanbanbanbanbanbtgcanbanbanbanbanbanbanbanbanb 114 666 CIGGAGGGATGTCCTTGTTGGTGGCCTCCTGCACTGGTGGCTGCCCTC 717 g ò

Terbib. Notice Notice of the period of the proteins of the protein of the pro 05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
SAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss. /*teg= a /note= "this sequence represents '2'; 2 can be a sequence of 6, 9 or 12 nucleotides (see Location/Qualifiers 01-FEB-1994; U00977. 01-FEB-1993; US-013416. 30-DEC-1993; US-176500. 31-JAN-1994; US-189331. UXNC.) UNIV NORTH CAROLINA. FOWINES DM. RAY BK; WPI; 94-279739/34 Q70468 standard; DNA; 114 BP. 55..60 P-PSDB; R65154 misc_feature 18-AUG-1994. Synthetic. RESULT

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peptide between the 2 domains. The oligonuclectides are also designed that the expressed peptide contains 2 or 4 cysteine residues positioned to, or flanking, the unpredicted or variant residues. These residues conformational rigidity to the peptides. The TSARs conformational rigidity to the peptides. The TSARs or comparise, compilating a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eq. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eq. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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                                                                                                                                                                                                                                                                                                                                  843 TGGTTGTGGTCAGCCTCGCCCCAGGGTCAACGTCAGTGACAGGCTGGGCTTCCGTTCCAG 784
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SAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                          783 CICCICCICCITCAGACAGIGCIGIGGGGGICGGGCIITGAAGAAGICIGAG 732
                                                                                                                                                                                                                                              Length 114;
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Pred. No. 2.29e-04;
33; Mismatches 75; Indels
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Q70469 standard; DNA; 114 BP.
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(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
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Best Local Similarity 3.6%;
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30-DEC-1993; US-176500
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/note= "this
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WILLY 90-151319/LD.

The sequences candom nucleotide sequences encoding ligand binding domains - identified by screening library of vectors or peptide(s) and useful for gene therapy and diagnosis

Establishments: Page 15: 224pp; English and an appetide library.

The sequences given in Ti3610-13 represent oligonucleotides which were used in the generation of the DC43 TSAR random peptide library.

The sequence of amino acids encoded by these sequences are covered by the generic sequence. All 20 naturally occurring amino acids substantially random in sequence. All 20 naturally occurring amino acids care encoded by the variable coding region. Invariant nucleotides are positioned at particular sites in these nucleotides sequences to aid the positioned at particular sites in these nucleotides equences to aid the positioned at particular sites in these nucleotides of the conditions of the synthesised oligonucleotides. The fermini of each set of the oligonucleotides, the invariant nucleotides at the 5' termini are folsen to encode pairs of invariant nucleotides at the 5' termini are folsen to encode pairs of sites for by restriction enzymes which can function in the same buffer conditions are commercially available at high specific activity, are not complementary to each other to prevent self-ligation of the synthesised double stranded oligonucleotides and which require 6 or grantlenger of cleaving within the inserted double stranded souther to prevent self-ligation of the synthesised oligonucleotides sequences. The 3' termini invariant nucleotide sequences. The 3' termini documentation to double stranded sets of nucleotides to aid in an and conversion to double stranded sets of nucleotides to aid in an and conversion to double stranded sets of nucleotides to aid in an and conversion to double stranded sets of nucleotides to aid in an acide and conversion to double stranded sets o
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a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DC43 TSAR library generating oligonucleotide #2.

Cis-element: ligand: highly specific DNA binding domain; HSDB; human;
NF-kappa-B; regulatory domain; murine; homologue; IL-6; interleukin;
HLA class I gene; HLA-BD?; HLA-1; acute phase protein response;
Syngene; immune response; IL-8; IL-16; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                         893 TGCCTGGGCGGGGTCCGGCCTCAGGAAGAAGAGTGCGGGTATCCCATAAGTGGTTGTGGT 834
                                                                                                                                                                                                                                                                                                                                                                         1 tgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnabnnbnnbnnbnnbnnnnnnn 60
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Pred. No. 2.29e-04;
29; Mismatches 74; Indels
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/note- "Random peptide generating fragment"
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13..72
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Tl3611 standard; DNA; 81 BP.
                                                                                                                                                                                                                                                                  2.8%;
8.0%;
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96-151391/15.
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15-AUG-1995; US-515190.
(CYTO-) CYTOGEN CORP.
FOWLKES DM, ROGWell JD
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                         Mismatches 42; Indels
  Length 81;
 Score 33; DB 21;
Pred. No. 6.57e-04;
                        20;
Query Match 2.7%;
Best Local Similarity 19.5%;
Matches 15; Conservative
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- 766 IGICIGAAGGAGGAGGIGGAACGGAAGCCCAGCCIGICACIGACGIIGACCCIGGGG 825
- ò
- 65 nnvnnvnnaccacaacc 81 g
- 826 CGAGGCTGACCACAACC 842 õ

Search completed: Thu Nov 6 12:46:06 1997 Job time : 155 secs

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(FE)
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

Thu Nov 6 12:46:31 1997; MasPar time 638.42 Seconds 990.580 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-842-827-7 (1-1232) from US08842827.seq 1232 Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 .. STD Nmatch Post-processing:

Searched:

707517 segs, 256659390 bases x 2

Minimum Match 0% Listing first 45 summaries

Database:

EST-2915

1: EST1 2: EST2 3: EST3 4: EST4 5: EST5 6: EST6 7: EST7 8: EST8

9: EST9 10: EST10 11: EST11 12: EST12 13: EST13 14: EST14

15: EST15 16: EST16 17: EST17 18: EST18 14: EST19 20: EST20

27: EST21 22: EST22 23: EST23 24: EST24 25: EST25 26: EST26

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33: EST33 34: EST34 45: EST49 46: EST48 49: EST49 44: EST44

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97: EST99 94: EST94 95: EST95 96: EST96 97: EST99 2 103:EST103 104:EST104 7 108:EST108 109:EST109 2 113:EST113 114:EST114 7 118:EST118 119:EST119 2 123:EST128 124:EST129 7 128:EST128 129:EST129 133:EST133 134:EST134 138:EST138 139:EST139 143:EST143 144:EST144 100:EST100 101:EST101 102:EST102 103 105:EST102 103 105:EST102 106:EST106 107:EST107 108 116:EST105 107:EST107 108 116:EST105 116:EST107 108 120:EST105 117:EST117 118 120:EST105 121:EST117 118 120:EST105 121:EST105 121:E Database:

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179:EST179
184:EST184
189:EST189
194:EST194
175:EST175 176:EST176 177:EST177 178:EST178 180:EST180 181:EST181 182:EST182 183:EST183 185:EST185 186:EST180 191:EST191 192:EST192 193:EST193 195:EST193 195:EST195 196:EST195 197:EST195 197:EST195 196:EST195 197:EST195 197:EST195
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Variance 3.184; scale 3.601 Mean 11.465; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	zl25a07.rl Soares pre	25a07.sl Soares pr	2d08.rl Soare	sapiens partial c	6h03.rl Homo sapi	zm17h03.s1 Stratage	sapiens partial	103.sl Homo sapi	2d08.sl Soares pr	7h03.rl Strat	e04.rl Soare	106.rl Homo s	07.rl Homo s	104.rl Homo s	3g09.rl Soare	100.11 SOAL	1538R Mouse L	c09.rl Soare	z141g01.rl Soares pre	911.rl Soare	3d11.rl Soare	Ball.rl Soare	lalu.rl soares s	11.rl Homo sapie	IGUZ.II SOGIES PIT	man placenta	149a08 rl Homo sapie	HOMO	r86all.rl Homo sapi	Human placenta cDNA	149b06.sl Scares f	SIE	95909.11 nound sapt	81b05.rl Soares p	k48b02.rl Soares p	i50all.rl Homo sapi	u86e01.rl Homo sapi	dlO.rl Homo sapi	e74al0.rl Homo sapi	c18c09.rl Homo sapi	1773F Fetal h	d38all.sl Soares fo
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ALIGNMENTS

AA151344 610 bp mRNA 2125807.rl Soares pregnant uterus NbHPU 350932.5', AA151344 91719889 DEFINITION ACCESSION NID KEYWORDS RESULT LOCUS

148:EST148 149:EST149 153:EST153 154:EST154

10-DEC-1996 sapiens cDNA clone

EST Homo

US-08-842-827-7.rst

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/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
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2125a07.s1 Soares pregnant uterus NbHPU Homo sapiens CDNA clone
502932 3'.
AA149244
97719838
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40M13 fwd. from Amersham
High quality sequence stop: 336.
Location/Qualifiers
                      1034 ACCAGGAGTCTGGAGATGCCTGGGTAGCCTCAGCATTTGGAGGGGAACCTGTTCCCGTC 1093
                                                                                                                                                                                       478 ggtccccaaatatcnccttcttttatggggttaaggaagggaccgagatcagatagt 537
                                                                                418 accaggattctggagatgcctgggtagccctcagcatttggaggggaacctgttcccgtc 477
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358 caggaaccctgggctgatgggagcagtgagcgggctccgttgcccctgccctgcactgg 417
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Vertebrate: Butheria; Primates; Catarrhini: Hominidae; Homo.
1 (bases 1 to 495)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
Washlu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/sex="female"
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The Washu-Merck EST Project
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/lab_host="DH10B"
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/organism="Homo saplens"
/note="Organ: uterus; Vector: pT773-Pac; Site_1: Not I;
Site_2: Eco RI; lst strand cDNA was primed with a Not I -
oligo(dT) primer [5'
AACTGGAAGAATTGGGGGCGCTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT773 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                   Washington naviety School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: est@wastson.wustl.edu
Finis clone is available royalty-free through LLNL; contact the
IMAGE Consortium info@image.lln.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 452.
Location/Qualifiers
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                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Petrefebrate, Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 610)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Huttman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P.
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/dev_stage="adult"
/lab_host="DH10B"
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WashU-Merck EST Project
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Matches 590; Conservative
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Washington University School of Medicine
Washington University School of Medicine
Mashington University School of Medicine
Mashington University Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Fax: 314 286 1810
Exai: 314 286 1810
Exai: alt 486 1810
Exail: est@watson wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28Mi3 rev2 from Amersham
High quality sequence stop: 237.
Location/Qualifiers
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Busaryotee mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 404)
1 (lark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Teraskis, E., Materston, R., Williamson, A., Wohldmann, P. and
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م
    Length 495;
                           0; Mismatches 22; Indels
  Score 396; DB 189;
Pred. No. 0.00e+00;
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ch 32.1%;
1 Similarity 93.8%;
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Genexpress.

Direct Submission
Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                      'n
                 /note-"Organ: uterus; Vector: p17T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tggagaaggtgtgcaggggaaaccctnttgatgtcaccgaggccaggttgtcttctact 120
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Bukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Butheria; Primates; Catarrhini; Hominidae; H
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H. sapiens partial cDNA sequence; clone c-1ge10.
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Pred. No. 0.00e+00;
0; Mismatches 8;
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Best Local Similarity 97.3%;
Matches 394; Conservative
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/organism-"Homo sapiens"
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Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Behar, G., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lany, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Poullot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
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                                                                                                                                             Clone library from B.Soares, Psychiatry Dept. Columbia University USA;
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 349;
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/isolate="muscular atrophy patient"
//dev.stage="3 months old"
//tissue_type="total brain"
//clone_lib="normalized infant brain cDNA"
/sex="Female"
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Homo sapiens cDNA clone 136661 5'
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Pred. No. 0.00e+00;
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Genexpress_library_idt: C;
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                                                                                                                                                                                                                                                                                                                                                                   significant homology found with
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Stretch_removed: nothing
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Homo sapiens

Bucaryotae, Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases I to 413)

Hilliar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Nucaba, T., Le, M., Lennon, C., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 9 AA074521 367 bp mRNA EST 07-OCT-1996 EM17h03.s1 Stratagene pancreas (#937208) Homo sapiens CDNA clone 525941 3'. High quality sequence stops: 251
Source: IMAGE Consortium, LLN.
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information. 300 658 61 aacaccactggagcgatgtccttgttggcctcctgcaggggggcactggtggcgcctca 120 718 240 838 9 Gaps 1 tecagitetteetggiggeetitgeeetetacgigggetacacegegigtetgaitaea 659 AACACCACTGGAGGGATGTCCTTGTTGGCCTCCTGCAGGGGGCACTGGTGGCTGCCTCA aggagctggaacggaagcccagcctgtcactgacgttgaccctgggggggagggtgaccac 779 AGGAGCTGGAACGGAAGCCCAGCCTGTCACTGACGTTGACCCTGGGGCGAGGCTGACCAC 241 aaccacttatgggatacccgcactcctcctgagggccggaccccgccaggnagggg 599 rccagrrcrrcregregecrrrreccrcraceregecraceceeergrerara agotgotgttgagttncagttnagggcccacccaggtggttccttncagcctng 354 WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu .. Length 413; Score 297; DB 21; Length 41 Pred. No. 0.00e+00; 0; Mismatches 10; Indels 93 t

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vector:
     9565475
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ECORI: Site_2: XhoI: Cloned unidirectionally. Primer:
Oligo dr. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Enail: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40N13 fwd. from Amersham
High quality sequence stop: 194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1094 GGACGGGAACAGGTTCCCCTCCAAATGCTGAGGGCTACCCAGGCATCTCCAGACTCCTGG 1035
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                                                 Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 367)
Hillier, L. Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 tgtgaaacaggtgccctattttactaaaaacacatatacattacatttacaaaacagc
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                                                                                                                                                                                                                     Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone=155941
/clone=11b="Stratagene pancreas (#937208)"
/lab_host="SOLR cells (kanamycin resistant)"
complement(<1..>367)
107 c 97 g 70 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 277; DB 178;
Pred. No. 0.00e+00;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCA-GCTGG-ACTCACAGCTCCCT-GCCTGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGAGTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Best Local Similarity 96.2%;
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   1..367
                                  Homo sapiens
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BASE COUNT
                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                   TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
                                                                                    REFERENCE
                                                                                                     AUTHORS
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21-SEP-1995

HSCIGE102 264 bp RNA EST H. sapiens partial CDNA sequence; clone c-1ge10. 239680

DEFINITION

RESULT

ACCESSION

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Direct Submission
Submitted (24-0CT-1994) Genethon, B.P. 60, 91002 Evry Cedex France
Submitted (24-0CT-1994) Genethon, B.P. 60, 91002 Evry Codex France
B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directionally
                                                                                                                                                                                                                                                                                                                                                                                                                              Aufiray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone library from B. Soares, Psychiatry Dept. Columbia University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1209 AACAGGIGCCCTATITIACTAAAAACCACATATACATTATACATTITACAAAACAGCAACTA 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1149 TCTGATCTCTCGGTCCCTTCCTTAACCCCATAAAAAGAAGGGGATATTTGGGGACCGACG 1090
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                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 264)
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95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stretch_removed: 18 T removed at sequence 5'end
Normalization_method: Bento Soares, P.N.A.S in press;
Genexpress_library_idt: C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 264;
partial cDNA sequence; transcribed sequence fragment.
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /isolate-"muscular atrophy patient"
/dev_stage-"3 months old"
/tissue_type-"total brain"
/clone_lib-"normalized infant brain cDNA"
/sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing_method: single read, full automatic;
Primer: (-21)M13_universal;
cDNA sequence complementary to mRNA (3'end)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 255; DB 105;
Pred. No. 0.00e+00;
0; Mismatches 5;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Senexpress_sequence_idt: alc-lge10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No significant homology found with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                         The Genexpress cDNA program
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larity 98.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 264)
fray, C., Behar, G.
                                                                                                                                                                                                                                                                                                       (bases 1 to 264)
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                                                                          Homo sapiens
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zml7h03.rl Stratagene pancreas (#937208) Homo sapiens CDNA Clone
525841 5'.
AA102178
91646351
                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd marsham
High quality sequence stop: 144.
Location/Qualifiers
   zk52d08.sl Soares pregnant uterus NDHPU Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: uterus; Vector: p1713-Pac; Site_1: Not I. Site_2: Eco RI; 1st strand cDNA was primed with a Not : oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1232 TITITITITITITITITIGEGAACAGGIGCCCTATITIACIAAAACCACATATACAT 1173
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                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Peterbarda: Butheria; Primates; Catarrhini; Hominidae; Homo. [ tases 1 to 167) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Huthman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Wanterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 tttttttttttttttttttgtgaaacaggtgccctattttactaaaaaccacatatacat
                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares pregnant uterus NbHPU"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 161; DB 137;
Pred. No. 2.28e-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_tin_____/ex-female"
/dev_stage="adult"
/lab_host="DH108"
complement(<1..>167)
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                                                                                                                                                                                                                                      The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="486447"
                                                                                                                                                                                                                                                                                  Contact: Wilson RK
WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.1%;
Best Local Similarity 100.0%;
Matches 161; Conservative
                                                                                                 Homo sapiens
                    486447 3'
AA044400
                                                  91522275
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                                                                                  human.
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BASE COUNT
   DEFINITION
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JOURNAL
COMMENT
                                 ACCESSION
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KEYWORDS
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                                                                                                                                                   Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 237)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                             02-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 gggggcagcggagccgctccactgntcccatcagcccagggnttct
                                                                           237 bp mRNA EST
Homo sapiens cDNA clone 136661 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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Pred. No. 3.44e-233;
0; Mismatches 8;
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969 CGTCCAGAACCCTCAGTGCCT 949
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65 c
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Best Local Similarity 95.1%;
Matches 215; Conservative
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9791779
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                                                                                         DEFINITION
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JOURNAL
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                                                            RESULT
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Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="441150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex-"unknown"
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Local Similarity 69.1%;
es 190; Conservative
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127 c
                                                          Unpublished (1996)
                                                                                                                                                                                                                                                                   MGI:266486
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(L'bases 1 to 511)

Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: pancreas, Vector: pBluescript SK-; Site_1: BCORI; Site_2: XhOI; Cloned unidirectionally. Primer: Oligo dT. Pancreatic adenocarcinoma cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATICGGCACGAG 3' -3' adaptor sequence: 5'
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 100.
Location/Qualifiers
1.177
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mg99e04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
AA008968 ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 acgggetcatggctggggtcaccatcacggccaccgtcatccttgtctcggccggggaan 120
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                                              Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 177)
Hilliar.L., Clark,N., Dubque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Unpublished (1995)
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="525941"
/clone_lib="Stratagene pancreas (#937208)"
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9
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Pred. No. 7.99e-185;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
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Best Local Similarity 96.0%;
Matches 170; Conservative
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                                                                                                                                                                                                                                             Contact: Wilson RK
                                    Homo sapiens
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                                    ORGANISM
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13], on equal amounts of mRNA from 2 13.5ppc and 2 14.5ppc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 j double-stranded chorn was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Patima Bonaldo.
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                                                                                                                                                                                  #444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mousest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 ccaactgtgacgtcactccagtggtgtttgtagtcagacactcgagaaaggcccacatat 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 atggaaaaagcaatgagcccaaactggagcatgggtcgtaagagtcttgcccagtctccc 386
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                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand
Seq primer: ETPTimer
High quality sequence stop: 325.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K97295 423 bp mRNA EST
yq74h06.rl Homo sapiens CDNA clone 201563 5'.
R97295
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Pred. No. 2.94e-103;
0; Mismatches 85;
                                                                                                         Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 TGTCCCGAGTAGAAAGACAACCTGGCCTCGGTGAC 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
Waterston, R.
The WashU-HHMI Mouse EST Project
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chomata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Cararrhini; Hominidae; Homo.
1 (bases 1 to 490)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 385

Source: IMAGE Consortium, LLNL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 gtggcactttatettcaagccaggatgaagggagactgggcaagactctacgccccaca 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 TIGGCGCIGIATGIGCAGGCACGACTCTGTIGGAAGIGGGCACGGCTGCTGCGACCCACA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 ctgcaatttggtcttgttgccgtatccatttatgtgggcctttctcgagtttctgattat 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     658 AAACACCACTGGAGCGAIGTCCTIGIIGGCCTCCTGCAGGGGGCACTGGTGGCTGCCCTC 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 GAGGCCAGGTIGICTTTCTACTCGGGACACTCTTCCTTTGGGATGTACTGCATGGTGTTC 537
                                                                                                 human clone=265309 primer=17 library=Soares melanocyte 2NbHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 95; DB 92;
Pred. No. 2.29e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 gttgctgtatatgtatcggatttcttcaaag 377
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Best Local Similarity 67.5%;
Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
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    CE02068 ; .
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EST.
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                             ACCESSION
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                                         LOCUS N31047 490 bp mRNA EST 10-JAN-1996 DEFINITION yx51h07.rl Homo saplens cDNA clone 265309 5' similar to WP:T28D9.3
                                                                                                                                                                                                                                                                                                                   Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammaila; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 423)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulliar,M., Hullian,M., Kucabb,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F., Tar,F., Tar,F., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
WashD-Merck EST Project
WashD-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Eax: 314 286 1810
Enail: est@watson.wustl.edu
High quality sequence stops: 301
Source: IMAGE Consortum, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (inf@@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 ctgcaatttggtcttgttgccgtatccatttatgtgggcctttctcgagtttctgattat 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598 GICCAGIICIICCIGGIGGCCIIIGCCCICIACGIGGGCIACACCCGCGIGICICAIIAC 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 aaacaccactggagcgatgtgttgactggactcattcagggagctctggttgcaatatta 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 GAGGCCAGGTTGTCTTTCTACTCGGGACACTCTTTCGGGATGTACTGCATGGTGTTC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658 AAACACCACTGGAGCGAIGICCITGITGGCCICCIGCAGGGGGCACTGGTGGCTGCCCTC 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 gaaggcaggttgtncttctattcaggncactcttcgttttncatgtactgcatgctgttt 71
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Bukaryotae: Metazoa, Bumetazoa, Bilateria, Coelomata,
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Pred. No. 3.95e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/clone="201563"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 gttgctgtatatgtatcggatttcttcaaag 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   718 ACTGTCTGCTACATCTCAGACTTCTTCAAAG 748
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Best Local Similarity 67.2%;
Matches 182; Conservative
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 agtcagtccctgactgacatttgccaagtattcaataggcagactgcggcctcacttctt 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 ggatgtttgtgatccagattggtcaaaaatcaactgcaagcgatggttacattgaatact 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 AGCCGTCTGCGACCCCGACTGGAGCCGGGTCAACTGCTCGGTCTATGTGCAGCTGG-AGA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 acatatgtcgagggaatgcagaaagagttaaggaaggcaggttgtccttctattcaggcc 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 AACAACTACGTGGCTGCTGTATACAAGGTGCTGGGGGACCTTCCTGTTTGGGGCTGCCGTG 327
                                                                                                                                                                                                                                                   Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata; Pertebrateis Eutheria; Primates; Catarrhini; Hominidae; Homo. [ Cases 1 to 472)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Rifkin,L., Roblifing,T., Soares,M., Parsons,J., Rifkin,L., Roblifing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 114; Length 47:
Pred. No. 3.14e-58;
0; Mismatches 127; Indels
                     635
  599 TCCAGTTCTTCCTGGTGGCCTTTGCCCTCTACGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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High quality sequence stop: 339.
Location/Qualifiers
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Best Local Similarity 62.1%;
Matches 211; Conservative
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Ammiota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 446)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 TGGGGACCTTCCTGTTTGGGGCTGCCGTGAGCCAGTCTCTGACAGACCTGGCCAAGTACA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 TGATTGGGCGTCTGAAGCCCCAACTTCCTAGCCGTCTGCGACCCCGACTGGAGCCGGGTCA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 actgctctgaaggctacattcagaactacagatgcagaggtgatgacagcaaagtccagg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGCTCGGTCTATGTGCAGCTGGAGAAGGTGTGCAGGGGAAACCCTGCTGATGTCACCG 478
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                     26-MAY-1995
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Feb: 314 286 1800
Fax: 314 286 1810
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                446 bp mRNA EST Homo sapiens cDNA clone 139351 5'
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Pred. No. 3.28e-62;
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High qality sequence stops: 153
Source: IMAGE Consortium, LLNL
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1 Similarity 60.8%;
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g	406	406 agggagactggggcaagactcttacgccccacactgcaatt 445

⁵⁰⁶ ACTCTTCCTTTGGGATGTACTGCATGGTGTTCTTGGCGCTGTATGTGCAGGCACGACTCT 565

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Search completed: Thu Nov 6 12:58:09 1997 Job time: 698 secs.

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Thu Nov 6 12:58:35 1997; MasPar time 336.04 Seconds 1007.529 Million cell updates/sec
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                                                                                                                                                                                         n.a. - n.a. database search, using Smith-Waterman algorithm
Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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(1-1232) from US08842827.seq
1232
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

Result

No. Score Match Length DB ID Description Pred.
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yv31b01.rl Scares fetal liver spleen lNFLS Homo sapiens cDNA clone 244297 5' similar to WP:T28D9.3 CE02068 ;.
                                                                                                                                                                                                                                                                                                  61 gattttactgcggggatgactccatccggtacccctaccgtccagataccatcacccacg 120
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                                                                                                  Eukaryotas, mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 478)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 0.00e+00;
0; Mismatches 26; Indels
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WashU-Merck EST Project
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Best Local Similarity 93.6%;
Matches 440; Conservative
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                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1237 Std Error: 0.00
Seq primer: mi3 -40 forward
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   MO 63108
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/lab_host="DH10B (ampicillin resistant)".
complement(<1...>491)
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143 c 142 g 100 t
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Pred. No. 0.00e+00;
0; Mismatches 4; Indels 4
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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Local Similarity 98.4%;
des 486; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                          419
tggccaagtacatgattgggcgtctgaggcccaactttctagccgtctgcgaanccgact 360
                                                                                        465
                                                                                                                                                                                                          AA107326 385 bp mRNA EST 04-FEB-1997 m1955h0.r1 Stratagene mouse kidney (#937315) Mus musculus CDNA clone 519739 5' similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN ;.
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                                                                                    407 GGAGCCGGGTCAACTGCTCGGTCTATGTGCAGCT-GGAGAAGGTGTGCAGGGGAAACCCT
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Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/clone_lib="Stratagene mouse kidney (#937315)"
                                                                                                                    Length 385;
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Pred. No. 3.53e-46;
0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="females"
/dev_stage="4 weeks"
/lab_host="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
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Location/Qualifiers
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Similarity 62.5%;
178; Conservative
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                   house mouse.
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/note-lorgan: brain; Vector: pSPORTI; Mouse Ventral
Midbrain directional cDNA library in pSPORTI. The library
was created by subtractive hybridisation using VM mRNA as
the target nucleic acid population and total cerebellar as
cDNA as the driver nucleic acid population. The clones are
/clone="spm221:25"
/clone="spm221:25"
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Robertson Laboratory of Biotechnology
Institute of Biomedical and Life Sciences, Division of Molecular
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                  248 tcaagggaatgaagagaaagtcaaggagggcaggttgtctttctactcgggacactcttc 307
gtccttgactgacatcgctaagtatactataggcagtttgcggccga-cttcttggctat 187
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309 Mousee VM cDNA library Mus musculus cDNA clone spmp22 1.25.
91816979
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Stewart, G.J., Savioz, A. and Davies, R.W.
Sequence analysis of 497 mouse brain ESTs expressed in Substantia nigra
Genomics 39, 147-153 (1997)
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<1..>337
112 c 83 g 83 t
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Fax: 44 141 330 5102/4878
Email: 9pga21@ddcf.gla.ac.uk
Seq primer: T/T3alpha
High quality sequence stop: 337.
Location/Qualifiers
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/organism="Homo sapiens"
/note="Organ: heart; Vector: pr7T3D (Pharmacia) with a modified polylinker; Sitel=1: Not I: Site=2: Eco RI: 1st strand CDNA was primed with a Not I - oligo(dT) primer [5/firaccarcreaagGGGGGGCGCATCIITITITITITITITI 3/],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Lenglin; 774 Std Error: 0.00
Seq primer: mob.REGA+Er
High quality sequence stop: 336.
Location/Qualifiers
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       268 AACAACTACGTGGCTGCTATACAAGGTGCTGGGGACCTTCCTGTTTGGGGCTGCCGTG 327
                                                                                                                                                                                                               M30942 564 bp mRNA EST 25-NOV-1996
2c64f09.rl Soares fetal heart NDHH19W Homo sapiens CDNA clone
327113 5' similar to WP:T28D9.3 CE02068 ;.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hallman,M., Rucabb,T., Leh,M., Hennon,C., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
WashUngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1800
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/clone_lib="Soares fetal heart NbHH19W"
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Best Local Similarity 60.9%;
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/clone="spmp21:22"
/clone="spmp21:22"
/clone="spmp21:22"
/clone="spmp21:22"
/clone="spmp21:22"
/clone=lib="Nouse VM cDNA library"
/tissue_type="ventral midbrain"
/lissue_type="ventral midbrain"
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Robertson Laboratory of Biotechnology
Institute of Biomedical and Life Sciences, Division of Molecular
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                       181 tggcaggatttgcccaaggagctctggtggcctgctgcatagtgttcttcgtgtccgacc 240
121 tggccttctacacgggattgtcacgggtatctgactacaagcatcatcctagcgatgtcc 180
                                                                                                                        680 TIGTIGGCCTCCTGCAGGGGCACTGCTGCCCCCCCTCACTGTCTCAGACT 739
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Sequence analysis of 497 mouse brain ESTs expressed in the
substantia nigra
Genomics 39, 147-153 (1997)
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Fax: 44 141 330 5102/4878
Eax: 44 141 330 5102/4878
Eaxil: gbga21gudcf.gla.ac.uk
Seg primer: T7/T3alpha
High quality sequence stop: 422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHz19W."
                                                                                                                                                                                  430
                                                                                                                                                                                                                                                                                          tgcctccttctccatgtacactatgctggaatttggtgctatanctgcaggcccgcttca 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Materston R., Williamson A., Wohldmann P., Wilson R.;
"The WashU-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contect: Wilson RK WashU-Merck EST Project Washington University Contect: Wilson RK WashU-Merck EST Project Washington University Mo 63108 Tel: 314 286 1801 Email: estéwatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. insert Length: 774 Std Error: 0.00 Seq primer: Rey Location/Qualifiers
                       AGCCAGTCTCTGACAGACCTGGCCAAGTACATGATTGGGCGTCTGAAGCCCAACTTCCT-
                                                                          aagtgtctgcaaccctgatttcagccagatcaactgctctgaaggctacattcagaacta
                                                                                                                            387 AGCCGTCTGCGACCCGACTGGAGCCGGGTCAACTGCTCGGTCTATGTGCAGCTGGAGAA
                                                                                                                                                                                  cagatgcagaggtgatgacagcaaagtccaggangccaggaagtccttcntctctggcca
                                                                                                                                                                                                                                   447 GGTGTGCAGGGAAACCCTGCTGATGTCACCGAGGCCAGGTTGTCTTTCTACTCGGGACA
                                                                                                                                                                                                                                                                                                                                        507 cretrecerrateracraceargraterit-eccercrareraceagacter
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7-MAY-1997 (Rel. 51, Last updated, Version 2)
2C64f09.rl Scares fetal heart NbHH19W Homo sapiens CDNA clone
327113 5' similar to WP:T28D9.3 CE02068 ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares fetal heart NbHH19W"/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <1..>564
BP; 128 A; 155 C; 139 G; 134 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                            491 cttggcgaggagc-cgnctgctncgggccctcctgcagtt 529
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; RNA; EST; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished.
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HS942332
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                                                                                                                                                                                                                                                                                       431
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Score 59; DB 88; Length 564; Pred. No. 6.47e-38;

4.8%;

Best Local Similarity

Query Match

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Anotes Organ: brain; Vector: pSPORT1; Mouse Ventral Midbrain directional cDNA library in pSPORT1. The library was created by subtractive hybridisation using VM mRNA as the target nucleic acid population and total cerebellar as CDNA as the driver nucleic acid population. The clones are /clone*spm221.23*
/clone*spm221.23*
/clone*lib**Mouse VM CDNA library*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Robertson Laboratory of Biotechnology
Institute of Biomedical and Life Sciences, Division of Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                 310
                                                                                                                                                                       328 AGCCAGTCTCTGACAGACCTGGCCAAGTACATGATTGGGCGTCTGAAGCCCAACTTCCT- 386
                                                                                                                                                                                                                                311 aagtgtetgcaaccetgattteagceagateaactgetetgaaggetacatteagaacta 370
                                                                                                                                                                                                                                                                                         387 AGCCGTCTGCGACCCCGACTGGAGCCGGGTCAACTGCTCGGTCTATGTGCAGCTGGAGAA 446
                                                                                                                                                                                                                                                                                                                                                  371 cagatgcagaggtgatgacagcaaagtccaggangccaggaagtccttcntctctggcca 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgeeteetteteeatgtaeactatgetggaatttggtgetatanetgeaggeeegettea 490
192 aacccctacgtggcagcactctataagcaagtgggctgcttcctctttggctgtgca-tc 250
                            507 CTCTTCCTTTGGGATGTACTGCATGGTGTTCTT-GGCGCTGTATGTGCAGGCACGACTCT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W39815 242 bp mRNA EST 05-FEB-1997
308 Mouse VM cDNA library Mus musculus cDNA clone spmp22 1.23.
W39815
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                                                                                                              251 agccagtctttcacagacattgccaaagtgtccatagggcgcctgcgtcctcacttcttg
                                                                                                                                                                                                                                                                                                                                                                                                           447 GGTGTGCAGGGGAAACCCTGCTGATGTCACCGAGGCCAGGTTGTCTTTCTACTCGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 242)
Stewart, G.J., Savioz, A. and Davies, R.W.
Sequence analysis of 497 mouse brain ESTs expressed in t
substantia nigra
Genomics 39, 147-153 (1997)
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Pred. No. 1.94e-34;
0; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="ventral midbrain"
<1..>242
82 c 60 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 cttggcgaggagc-cgnctgctncgggccctcctgcagtt
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/organism="Mus musculus"
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Tel: 44 141 330 5102
Fax: 44 141 330 5102/4878
Email: gbga21@udcf.gla.ac.uk
Seq primer: T773alpha
High quality sequence stop: 2.
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I Similarity 61.6%;
149; Conservative
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Best Local Similarity
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Gaps

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5 gtcaaggagggcaggttgtctttctactcgggacactcttcattctctatgtactgcatg 64
               Length 87;
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83 A; 58 C; 85 G; 87 T; 0 other;
               Score 47; DB 33; Le
Pred. No. 2.62e-24;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.,
"The WashU-HHMI Mouse EST Project";
                                                                                                                                                                                      MM1155742 standard; RNA; EST; 313
AA237956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="692496"
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larity 69.4%;
Conservative
               3.8%;
larity 80.5%;
Conservative
                                                                                                                                                  532 GIGITCIIGGCGCTGIA 548
                                                                                                                                                                                                                                                                                                                            musculus (house mouse)
                                                                                                                        81
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                                                                                                                        65 ctgtgtgtcgcacttta
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es 84; Conser
                          Local Similarity
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                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished.
                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              m185a07.rl Stratagene mouse kidney (#937315) Mus musculus cDNA clone 518772 5' similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                    619
                                                    getteacetggcgcggggcccgactgetccgcccctcctgcagttcactttgctcatga 120
                                                                                                                                                                           680 TIGITGGCCTCCTGCAGGGGGACTGGTGGCTGCCTCACTGTCTGATCTCAGACT 739
                 121 tggccttctacacgggattgtcacgggtatctgactacaagcatcatcctagcgatgtcc
                                                                                                                                                         181 tggcaggatttgcccaaggagctctggtggcctgcatagtgttcttcgtgtccgacc
 cgggccacgcctccttctccatgttcactatgctgtatctggtgctctaccttcaggccc
                                                                            560 GACTCTGTTGGAAGTGGGCACGCTGCTGCGACCCACAGTCCAGTTCTTCCTGGTGGCCT
                                                                                                                                 620 TIGCCCICIACGIGGCIACACCCGCGIGTCTGATIACAAACACCACTGGAGCGAIGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene mouse kidney (#937315)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 revl Er from Amersham
High quality sequence stop: 55.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex-"females"
/dev_stage-"4 weeks"
/lab_host-"SOLR (kanamycin resistant)"
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Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"/strain="C57/B16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
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JOURNAL
ч
                                                    61
                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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06-MAR-1997 (Rel. 51, Created)
Version 1)
MX/8907.rsl. 51, Last updated, Version 1)
MX/8901.r1 Soares mouse NML Mus musculus cDNA clone 692496 5'
similar to TR:G1161100 G1161100 HYDROGEN PEROXIDE-INDUCIBLE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marze M.Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Moshington University School of MedicineP 4444 Forest Park Parkway, Emails: W. St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Emails: mouseest@waspon.wustl.edu This clone is available royalty-free through LLE.; contact the IMAGE Consortium (info@image.llnl.gov) for further information. NOI:426056 Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 57.
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                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson
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Pred. No. 6.44e-19;
0; Mismatches 36; Indels
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61 catatatggaaaaagcaatgaggccaaactggagcaatggtcgtaagaagcctggccaat 120
                GTGGCTGCCCTCACTGTTGCTACATCTCAGACTTCTTCAAAG 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 415 BP; 124 A; 87 C; 86 G; 116 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3%; Score 41; DB 87; I
Best Local Similarity 69.9%; Pred. No. 7.27e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                  standard; RNA; EST; 415
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07-MAR-1997 (Rel. 51, Last upda
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                                                                                                                                                                                                                                                                                                          1 (bases 1 to 313)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                    Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     691 GGAGGCCAACAAGGACATCGCTCCAGTGGTGTTTGTAATCAGACACGCGGGTGTAGCCCA 632
           catatatggaaaaagcaatgaggccaaactggagcaatggtcgtaagaagcctggccaat 120
                        ggagtccaactgtgacgtcactccagtggtgtttgtagtcagacactcgagaa-aggcca 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
FSR: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 57.
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Washington University School of MedicineP
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Pred. No. 6.44e-19;
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/clone_lib="Soares mouse NML"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
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/lab_host="DH10B"
<1..>313
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llarity 69.4%;
Conservative
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Best Local Similarity (
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                                                                                                                                                                                                                                           house mouse.
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                                                              121 t 121
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/Organism="Homo sapiens"
//Organism="Homo sapiens"
//Organism=
//Organ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, School of Medicine 1810 Email: estGwatson.wustl.edu This Clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 773 Std Error: 0.00 Seq primer:
07-MAR-1997 (Rel. 51, Last updated, Version 2)
2b63f08.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 308295
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Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Rucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rikin L., Rohlfing T., Tan F., Trevskis E.,
Waterston R., Williamson A., Wohldmann P., Wilson R.;
"washu-Merck EST Project";
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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13

RESULT

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/organism="Drosophila melanogaster"
/note="Organ: embryo; Vector: plasmid: Site_1: Clai;
Site_2: Fail: mRNA purified from rough endoplasmic
site_2: Fail: mRNA purified from rough endoplasmic
reticulum-bound polysomes was used as a template. cDNA's
directionally cloned at HinDIII and Pail in Bluescript
SKt Cloned into HinDIII, but the site was destroyed to
add an adapter sequence. So Clai is now the restriction
enzyme at site I of vector. Primers - 5' universal, 3'
ml3-20 (reverse), 3' T3, 5' T7"
/clone_1Db="Drosophila Embryonic Polysomal in pBS skr"
/sex="maile and female"
/dev stage="0" to 24 hours old embryo"
/lab_host="Xil Blue MRF"
                                                               Kopczynski,C., Serrano,T., Rubin,G. and Goodman,C. mRNAs enriched for membrane and secreted proteins versus cytosolic
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2p52f10.s1 Stratagene HeLa cell s3 937216 Homo saplens cDNA clone
613099 3'.
AA181403
97765128
                                                                                                                                                       Onpublished (1996)
Other ESTS: CK00216.5prime
Contact: Lewis, S.
Contact: Lewis, S.
Gondiar and Cell Biology
University of Berkeley
139 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: EST@fruitfly.berkeley.edu, http://fruitfly.berkeley.edu/
Insert Length: 422 Std Error: 0.00
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Location/Qualifiers
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Busaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 446)
1 (bases 1 to 446)
1 (bases 1 to 416)
1 (
   Muscomorpha; Ephydroidea; Drosophila
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Pred. No. 7.12e-09;
0; Mismatches 62; Indels
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91 c 102 g
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WashU-Merck EST Project
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Best Local Similarity 60.3%;
Matches 94; Conservative
                                      (bases 1 to 422)
                                                                                                                                      proteins
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BASE COUNT
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                        CK02248.contig Drosophila Embryonic Polysomal in pBS skr Drosophila melanogaster cDNA clone CK02248 complete.
                                                                                                                                                                                                                                                                                                                                                                                     Kopczynski,C., Serrano,T., Rubin,G. and Goodman,C. mRNAs enriched for membrane and secreted proteins versus cytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism--brosophila melanogaster"
/forde--Organ: embryo: Vector: plasmid; Site_1: ClaI;
Site_2: PstI; mark purified from rough endoplasmic
reticulum-bound polysomes was used as a template. CDNA's
directionally cloned at HinDIII and PstI in Bluescript
SKt. Cloned into HinDIII, but the site was destroyed to
add an adapter sequence. So ClaI is now the restriction
enzyme at site I of vector. Primers - 5' universal, 3'
/clone--CK02248*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Lewis, S.
G. M. Rubin-Molecular and Cell Biology
University of Berkeley
University of Berkeley
539 LSA, Berkeley,
Fax: 510 643 9947
Fax: 510 643 9947
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/sex="male and female"/
/dev_stage="0 to 24 hours old embryo"
/lab_host="XL1 Blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 atgcaatggaagcagttgagaatgctgtgccacctgctccagttcctgctgctcatgttc 599
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Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
   25-JAN-1997
                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
tracheata: Haxapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 914)
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Pred. No. 8.73e-11;
0; Mismatches 71; Indels
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   mRNA
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Best Local Similarity 59.7%;
Matches 105; Conservative
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                            DEFINITION
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TITLE
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
711: 314 286 1800
Fax: 314 286 1810
Fax: 
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Gaps ö 199 ttgaagaggtcagacacgaagaaaactatgcagcaggccaccaggggttcttgagcaaat 258

259 cctgccagaacatcactgggatggtgcttgtggtctgatacgcg 302

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å ç Search completed: Thu Nov 6 13:05:06 1997 Job time : 391 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 6.89 Seconds 492.650 Million cell updates/sec Tue Nov 4 10:32:20 1997; Run on:

Tabular output not generated.

Description: Perfect Score: Title:

>US-08-842-827-8 (1-276) from US08842827.pep 2118 1 MORRWVFVLLEDVLCLLVASL......KEEELERKPSLSLTLTLGRG 276 Sequence:

PAM 150 Gap 11 Scoring table:

101610 seqs, 12294212 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq28
lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Mean 34.064; Variance 157.795; scale 0.216

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Ouery Match	Ouery Match Length DB	DB	ID	Description	Pred. No.
1		4.7	882	6	R45749	Alpha-DNA polymerase	1.47e+01
8	97	4.6	317	6	W02661		2 016+01
m	97	9	317	19	R48689	Coupled	2.016+01
4	95	4.5	-	Н	R05233		2.73e+01
S	95	4.5	2020	7	R06584		2.73e+01
9	94	4.4	154	m	P50101	Sequence of a pure po	3.18e+01
7	94	4.4	154	~	R05175	Tumoricidal polypepti	3.18e+01
œ	94	4.4	154	m	P50138	Rabbit tumor necrosis	3.18e+01
0	94	4.4	154	7	R05190	Tumoricidal polypepti	3.18e+01
10	96	4.4	154	7	R03266	Rabbit tumour necrosi	3.18e+01
11	94	4.4	154	a	R05173	Tumoricidal polypepti	3.18e+01
12	94	4.4	156	æ	R41860	Rabbit TNF-alpha mute	3.18e+01
13	94	4.4	234	ო	P50139	Rabbit tumor necrosis	3.18e+01
14	94	4.4	234	ო	P50095	Sequence of a precurs	3.18e+01
15	94	4.4	235	7	P71180	Rabbit tumour necrosi	3.18e+01
16	93	4.4	638	7	R37325	Rat brain glycine tra	3.70e+01
17	92	4.3	154	ო	P50384	TNF analogue having m	4.31e+01
18	91	4.3	156	œ	R41856	Bovine TNF-alpha mute	5.01e+01
19	92	4.3	157	œ	R41858	Ovine TNF-alpha mutei	4.31e+01
20	92	4.3	158	4	R22126	Sequence of ovine tum	4.31e+01

4.31e+01 4.31e+01 5.01e+01 5.01e+01 4.31e+01	5.82e+01 5.82e+01 5.82e+01 6.76e+01 6.76e+01 1.05e+02	1.05e+02 9.105e+02 9.10e+01 9.10e+01 1.05e+02 1.05e+02 1.05e+02 1.05e+02 1.05e+02 1.05e+02
F-alpha. of ovine tootal heart indothelin coillic DNA pogenes NIAES	Protein encoded by Ro Human placenta short Human placenta long f gIV from BHV-1 strain Pemphigus vulgaris an Human pemphigus vulga Secretory signal sequ Secretory signal sequ Secretory cland	of tumour heroidin as heroidin as i uransmemb i urance o tokine, ST2 mour necros of tumour protease-2 protease I
R23665 R22129 R76236 R76226 R43996	R42506 W08370 W08371 R37684 W07908 R30742 P70041	P60527 W20650 W20650 W09639 P90424 P60530 W14481 W01791
444488	3 5 6 1 4 5 0 8 3 3 8 3 3 8 3 3 3 3 3 3 3 3 3 3 3 3	2222233
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22 23 25 25 26	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	88888444444 88888888888888888888888888

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12-NOV-1996 (first entry)
G-protein coupled human m2 muscarinic acetylcholine receptor.
G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine, cAMP; adenosine; thrombin, adrenergic; opsin; muscarinic acetylcholine; endochenin; bombesin; endocrine; rhodopsin; Romo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D 25-JAN-1994.

TO 25-JAN-1992. 194713.

R 30-JUN-1992; JP-14713.

R 30-JUN-1992; JP-14713.

R 17-1992; JP-147
                                                                                                                                                                                                                                     Alpha-DNA polymerase.

Clone: DNA polymerase; hybridise; amplification; genetic engineering; PCR; polymerase chain reaction; restriction map; plasmid.
Sulofolobus solfatarious.
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Pred. No. 1.47e+01;
12; Mismatches 4; Indels
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R45749 standard; Protein; 882 AA.
R45749;
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WO2661 standard; peptide; 317 AA.
WO2661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.4%;
Matches 14; Conservative
                                                                                                                                                                                 09-AUG-1994 (first entry)
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12 VLC-LLVASLPFAILTLVNAPYRRGFYGGDDSIRYPRRPDTITHGLMAGVIITATVIL
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19-SEP-1993; UGB528.
PARE 199-SEP-1995; UGB528.
AUTHORY NEW YORK STATE.
NUTRIPLY NEW YORK STATE.
NUTRIPLY NEW SCHURSTEN DI;
MURPHY NEW SCHURSTEN DI;
POLYPEPTIGE OF G-coupled receptor proteins (GPRs) - useful for bolypeptides of G-coupled receptor proteins selected from CAMP, adenosine, muscarinic acetylcholine, proteins verce used to design polypeptides, profeins selected from CAMP, adenosine, muscarinic acetylcholine, corput proteins were used to design polypeptides, pref based on the receptor proteins were used to design polypeptide receptor ligand binding assays. The polypeptide fragments retain biological activity such as Inding a RPR ligand binding to a GPR CS (see R48759-R48758, R50569-R50807) and R89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to Sequence 317 AA;
                                                                                                                                                   for treating schizophrenia
Disclosure; Column 49-52; 184pp; English.
Proteins N0265-W07210 represent a range of G-protein coupled receptor (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenegic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand blanding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding a compositions for treating subjects suffering from a pathology aused in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein coupled human mission acetylcholine receptor protein. G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 vvcdlyvvsna-svmnlliisfdr-yfcvtkpltypvkrttkmagmmiaaawvlsfil 121
                                                                                                                                      New dopamine receptor peptide - useful as antipsychotic agent, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 VLC-LLVASLPFAILTLVNAPYKRGFYCGDDSIRYPYRPDTITHGLMAGVTITATVIL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.6%; Score 97; DB 19; Length 317; Best Local Similarity 25.9%; Pred. No. 2.01e+01; Matches 15; Conservative 17; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 4.6%; Score 97; DB 16; Length 317; Best Local Similarity 25.9%; Pred. No. 2.01e+01; Matches 15; Conservative 17; Mismatches 23; Indels
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R48689 standard; Protein; 317 AA.
             16-APR-1996.
10-SBP-1992; 943236.
10-SBP-1992; US-943236.
09-SEP-1993; US-118270.
UVIY ) UNIV NEW YORK STATE.
MUZPHY RB, SCHUSTER DI;
WPI; 96-208785/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R48689;
OS-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   317 AA;
                                                                                                                                                                                                                                                                                                                                                                                  schizophrenia.
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WO9405695-A1.
US5508384-A
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                             Human lymphotoxin synthetic gene alterated to leave only one restriction enzyme recognition site altered to leave only one restriction enzyme recognition site bischosure; Fig 1.13pp; Japanese.

It is the same anino acid sequence as natural HL. Its encoding gene is genetically engineered to make modifications of HL easier and improved lymphotoxins can be prepd.
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The sequence deduced from CDNA derived from 3 overlapping clones, pRN3-1: pPRN4-2: Deposited as Arcc 678885, 67886, and pRN4-4: Deposited as Arcc 678885, 67886, and 67887 resp.) The clones were isolated from a cDNA library in the lambda Zap vector prepd. from mRNA obtd. from newborn rat hearts using rat brain II cDNA probe. The protein has diagnostic, therapeutic, and prognostic applications.
                                             03-AUG-1990 (first entry)
Human lymphotoxin (HL) encoded by new synthetic lymphotoxin gene
Human lymphotoxin (HL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 95; DB 1; Length 172;
Pred. No. 2.73e+01;
16; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.5%: Score 95; DB 2; Length 2020
Best Local Similarity 27.7%; Pred. No. 2.73e+01;
Matches 13; Conservative 15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences, polypeptides and peptides associated with proteins, useful as antiarrythmic and cardiotonic drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 gytsfdsfawaflalfrlmtgdcwerlygqtlrsagklym1ffmlv1 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 RPDIITHGLMAGVIITATVILVSAGEAYLVYTDRLYSRSDFN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 rantdraflqdgfslsnnsllvptsgiyfvysqvvfsrkays
                                                                                                                                                                                      27-OCT-1987; 271513.
27-OCT-1987; JP-271513, JP-287035
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R06584 standard; protein; 2020
R05233 standard; protein; 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 4.5%;
Local Similarity 26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cardiac sodium channel Rat; arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1990; U00768.
13-FEB-1989; US-310330
(ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90-275095/36.
                                                                                                                                                                                                                                                                                                WPI; 90-047988/07.
                                                                                                                                                                                                                                            (SANY) Sankyo Kk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus rattus.
WO9009391-A.
                                                                                                                                                                                                                                                                                                                            N-PSDB; Q93289
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                                                                                                                                J02000447-A
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66 vvcdlyvvsna-svmnlliisfdr-yfcvtkpltypvkrttkmagmmiaaawvlsfil 121

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Tumoricidal polypeptide(s) - in which DNA to code the polypeptide(s) is constructed from human-derived TNF-coding DNA and rabbit-derived TNF-coding DNA.
                                                                                                                                                                                                                                                                                                                                 New DNA encoding rabbit tumour necrosis factor - useful in expression of the factor in Escherichia coli for anti:tumour use claim 2; Page 39; 64pp; English.

The rabbit TNF can be obtained in large amounts by recombinant DNA techniques. DNA encoding rabbit TNF is obtained by cultivation of rabbit macrophages with inducers. A fraction containing TNF mRNA is separated from the macrophages and used for the preparation of a cDNA library. The TNF may be used as an antiutmor agent. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 94; DB 3; Length 154;
Pred. No. 3.18e+01;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94; DB 2; Length 154;
Pred. No. 3.18e+01;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 anallangmkltdnqlvvpadglyliysqvlfsgqgcrsyvllthtv 77
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The sequence is derived from tumour necrosis factor
See also R05173-76 and R05189.
                          Tumor necrosis factor; lymphokine; antitumor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-1990 (first entry)
Rabbit tumour necrosis factor polypeptide.
Umoricide, Tumour necrosis factor.
Oryctolaqus cuniculus.
J02019398-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OULT 9
R05190 standard; protein; 154 AA.
R05190;
18-JUL-1990 (first entry)
Tumoricidal polypeptide.
Tumoricide: Fumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R03266 standard; protein; 154 AA R03266;
                                                                                                                 26-JUN-1985.
27-NOV-1984; 114325.
02-DEC-1983; JP-228790.
(DAIN ) DAINIPPON PHARM KK.
Yamda M. FIRULANI Y, NOTAKE M;
WPI: 85-154142/26.
N-PSDB; N50196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.JAN-1990.
06-JUL-1988; 166913.
06-JUL-1988; JP-166913.
(ASAH) Asahi Chemical Ind KK.
WPI: 90-064642/09.
N-PSDB: Q02045.
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06-JUL-1988; 166913.
06-JUL-1988; JP-166913.
(ASAH) Asahi Chemical Ind KK.
Rabbit tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 29.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 4.4%;
Local Similarity 29.8%;
les 14; Conservative
                                                            Oryctolagus coturnix.
EP-146026-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA library. The N50197 and P50139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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AC RO
DT 18
DE RA
TU
KW TU
FON JO
PD 23
PP 06
PR 06
PR 70
NAME OF STREET O
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DNA and rabbit-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inducing necrosts of tunours and as antivirals of tunours of claim 1; Page 54; 65pp; English.

The TNEs of the invention are able to induce necrosis of tunours without toxic effects on the normal living body tissues. They are also antivirals. Dose is 50-100 x 1,000,000 units daily for an adult. The DNA is ligated to a replicable expression vehicle to give a recombinant DNA. This is used to transform a microorganism, transformants are selected and incubated to produce TNE. Specifically claimed are plasmids pTNF-lac-1 and pTHF-lacUV5-1 and identified and isolated after studies on rabbit TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide(s) having 154 aminoacid sequence - useful for
                                                  Sequence of a pure polypeptide having tumour necrosis factor (TNF) activity.
Antiviral agent; lymphokine; antitumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.4%; Score 94; DB 2; Length 154; Best Local Similarity 29.8%; Pred. No. 3.18e+01; Matches 14; Conservative 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 3; Length 154; Pred. No. 3.18e+01; 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 3; 11pp; Japanese.
The sequence is derived from tumour necrosis factor DNA.
See also R05173-76 and R05189-90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 THGLMA-GVIITATVILVSAGEAYLVYTDRLYSRSDFNNYVAAVYKV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S3 THGIMA-GVTITATVILVSAGEAYLVYTDRLYSRSDFNNYVAAVYKV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 anallangmkltdnqlvvpadglyliysqvlfsgqgcrsyvllthtv 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.JUL_1990 (first entry)
Tumoricidal polypeptide.
Tumoricide, Tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä.
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06-JUJ-1988; 166913.
06-JUJ-1988; 17P-166913.
(ASAH) Asahi Chemical Ind KK.
WPI; 90-064642/09.
N-PSDB: Q02035.
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P50138 standard; protein; 154 .
P50138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R05175 standard; protein; 154
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Best Local Similarity 29.8%;
Matches 14; Conservative
                                                                                                                                                                                                     17-JUL-1985.
07-MAY-1984; 105149.
26-DEC-1983; JP-251817.
08-FEB-1984; JP-019850.
18-ARR-1984; JP-076584.
(ASAH.) ASAHI KASEI KOGYO.
                          (first entry)
                                                                                                                                                Oryctolagus cuniculus
EP-148311-A.
                                                                                                                                                                                                                                                                                                                                                                                       Itoh H;
WPI; 85-172835/29.
N-PSDB; N50113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J02019398-A.
                          30-0CT-1991
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Gaps

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Gaps

1;

01-JAN-1980 (first entry)

RESULT ID P5 AC P5 DT 01

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Length 154;

DNA

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/label- Arg, Cys, Asp, Gln, Asn, Ser, Thr, Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 29.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                         12-MAR-1993; U02475.
12-MAR-1992; US-852625.
(WISN/) WISNIESKI B J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus coturnix.
                                                                                                                                   Misc_difference 120
                                                                                                  Misc_difference 118
                                                                                                                                                                                                                                                                                                                                                                                                                156 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; N50197
                                                                                                                                                                                                                                                                                          Wisnieski BJ;
                                                                                                                                                                                                                                               6-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P50139;
                                                                                          /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding the sequence is combined with DNA encoding a similar tumour necrosis factor DNA from humans to produce new tumoricidal polypeptides. See also R03265.
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                                                                                                                                   Ä
                                                                                                                                                                                                                                                                                                                                                       Tumoricidal polypeptide(s) - in which DNA to code the polypeptide(s) is constructed from human-derived TNF-coding DNA and rabbit-derived TNF-coding DNA.
          Tumoricidal polypeptide(s) - in which DNA to code the polypeptide(s) is constructed from human-derived TNF-coding DNA and rabbit-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1994 (first entry)
Rabbit TNF-alpha mutein with modified channel-forming activity.
Tumour Necrosis Factor alpha: TNF-a; target membrane permeability;
TNF trimer: lon channel; mutein; lapine.
Oryctolagus cuniculus.
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                                                                                                            Score 94; DB 2; Length 154;
Pred. No. 3.18e+01;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.18e+01;
14; Mismatches 18; Indels
                                                                                                                                                                     Disclosuré; Page 4; 11pp; Japanese.
The sequence 1s derived from tumour necrosis factor DNA
sea also R05174-76 and R05189-90.
Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S3 THGLMA-GVTITATVILVSAGEAYLVYTDRLYSRSDFNNYVAAVYKV 98
                                                                                                                                                       31 anallangmkltdnqlvvpadglyllysqvlfsgqgcrsyvllthtv 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 anallangmkltdnqlvvpadglyliysqvlfsgqgcrsyvllthtv 77
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/labol= Trp, Ser, Thr, Ala, Met, cys, Phe or Tyr
/labol= "wild-type channel residue is Leu"
Misc_difference 59
/labol= Trp, Ser, Thr, Ala, Met, Cys or Phe
Misc_difference 97
Misc_difference 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Arg, Cys, Glu, Asp, Gln, Asn, Ser, Thr
or His
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc_difference 11
/label- Glu, Arg, Cys, Asp, Gln, Asn, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "wild-type channel residue is Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "wild-type channel residue is Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualiflers
                                       Disclosure; Fig 1; 11pp; Japanese.
                                                                                                                                                                                                                                         18-JUL-1990 (first entry)
18-JUL-1990 (first entry)
Tumoricidal polypeptide.
JUROS1019398-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R41860; standard; protein; 156 AA. R41860;
                                                                                                                                                                                                                                                                                      23.7AN-1990.
06.7UL-1988; 166913.
06.7UL-1988; JP-166913.
(ASAH) Asahi Chemical Ind KK.
WPI, 90-064642/09.
                                                                                                                                                                                                           T 11
R05173 standard; protein; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4%;
Local Similarity 29.8%;
hes 14; Conservative
                                                                                                            Ouery Match
Best Local Similarity 29.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc_difference 111
                                                                                        154 AA;
WPI; 90-064642/09
                              TNF-coding DNA.
                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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855558877988
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WPI: 93-303462/38.

WPI: 93-303462/38.

Producing modified tumour necrosis factor alpha - useful for regulating modified tumour necrosis factor channel activity e.g.

Increasing permeability

Increasing permeability

Increasing permeability

Increasing permeability

Increasing permeability

The sequence of rabbit TNF-alpha disclosed in DNA 5:157-165,

Increasing permeability

Increasing permeability

Increasing the sequence of the specification. A modified version of this substituted (see Features Table). The resulting TNF-alpha mutein has modified channel activity compared to wild-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA encoding rabbit tumour necrosis factor - useful in expression of the factor in Escherichia coli for anti:tumour use claim 6; Page 39; 64pp; English.

The rabbit TNF can be obtained in large amounts by recombinant DNA rechiques. DNA encoding rabbit TNF is obtained by cultivation of rabbit macrophages with inducers. A fraction containing TNF mRNA is exparated from the macrophages and used for the preparation of a cbM library. The TNF may be used as an antiutmor agent. See also NSO196 and PSO138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 anallangmkltdnqlvvpadglyliysqvlfsgqgcrsyvllthtv 79
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Rabbit tumor necrosis factor precursor.
Tumor necrosis factor; lymphokine; antitumor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Trp, Ser, Thr, Ala, Met, Cys, Phe or Tyr /note- "wild-type channel residue is Ile" Misc_difference 156
/note- "wild-type channel residue is Met but in
human TMF-alpha the amino acid at the
Corresp. position is Lys"
Misc_difference 115
                                                                                                                                                         His
                                                                                                                                                                                                                                                                                           /label Trp, Phe, Ser, Thr, Ala, Met or Cys
/note= "wild-type channel residue is Tyr"
                                                                                                                                                         /label= Lys, Arg, Cys, Asp, Gln, Asn, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                         /label- Ala, Val, Ser or Thr
/note- "wild-type channel residue is Gly"
Misc_difference 154
                                                                                                                                                                                                                                "wild-type channel residue is Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Trp, Ser, Thr, Ala, Cys or Tyr
/note= "wild-type channel residue is Leu"
W09318148-A.
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P50139 standard; protein; 234 AA.
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02-DEC-1983; JP-228790.
(DAIN ) DAINIPPON PHARM KK.
Yamda M, Furutani Y, Notake M;
WPI: 85-154142/26.
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Disclosure; Table 2-2, Page 35; IO2pp; English.

Disclosure; Table 2-2, Page 35; IO2pp; English.

The inventors claim a DNA having or contg a base sequence corresp.

The inventors claim a DNA having or contg. a base sequence of having or contg. a base sequence corresp. to an AA sequence of formula: (Met)p-(X)n-(B)m-A in which A- a polypeptide of formula (Ia) in which one or more AAs may be deleted or replaced by other AAs;

B- Ser-Ser-Arag in which 1-3 of the AA residues may be deleted or replaced by other AAs;

C alaimed is a DNA contg. a base sequence different from but having replaced by other AAs; to the AA sequence of formula [Ia] is shown by the sequence of the bases nos. 286-738 in Table 4

KNSOG6). The base sequence shown in NSOI64 corresponds to the base sequence from the 37th to 738th bases in NSOI65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
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                                                                                                   Gaps
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Rabbit tumour necrosis factor precursor from plasmid pHTR91.
Cancer; antitumour; pHTP362.
    Score 94; DB 3; Length 234;
Pred. No. 3.18e+01;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amatch 4.4%; Score 94; DB 3; Length 234; Local Similarity 29.8%; Pred. No. 3.18e+01; les 14; Conservative 14; Mismatches 18; Indels
                                                                                                                                                                               111 anallangmkltdnglvvpadglyliysqvlfsgqgcrsyvllthtv 157
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                                                                                                                                                                                                                              7. 14
P50095 standard; Protein; 234 AA.
P50095;
06-0cT-1991 (first entry)
Sequence of a precursor of rabbit tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-528-1985, 102093.
26-FEB-1984, 19-043617.
23-APR-1984, JP-04863.
17-AUG-1984, JP-172307.
(DAIN ) DAINIPPON PHARM KK.
Yamada M, Furutani Y, Notake M, Yamagishi J;
WPI: 85-238092/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antitumour agent; cytotoxin; lymphokine. Oryctolagus cuniculus. Location/Qualifiers Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
82..235
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P71180 standard; Protein; 235 AA.
P71180;
Query Match
Best Local Similarity 29.8%;
Matches 14; Conservative
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J61294000-A.
24-DEC-1986.
21-JUN-1985; 136281.
21-JUN-1985; JP-136281.
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Protein
EP-155549-A.
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Matches
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DAC P7
AC P7
DT 22
DE RAB
NW CA CA
CA CA
FTH PR
PN J6
PD 24
PF 21
PR 21
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DR WPI; 87-039562/06.

DR N-PSDB; N71312.

PT New polypeptide and a DNA coding it - has anti-tumour activity
PS Disclosure; Fig 2: 14pp; Japanese.

C Claimed sequence is procured from phenocritical plasmid pHTD362,

CC Constructed from plasmid pHTR91. The gene product has antitumour

CC Sec also N71311.

SQ sequence 235 AA;

Query Match

4.4%; Score 94; DB 2; Length 235;

Best Local Similarity 29.8%; Pred. No. 3.180+01;

Matches 14; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

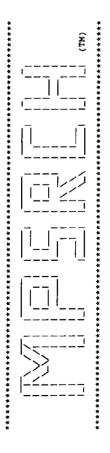
Agther 112 anallangmkitdnqlvvpadglyliysqulfsqqcrsyullthty 158

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Qy S3 THGLMA-GYTITATVILVSAGEAYLVYTDRLYSRSDFNNYVAAVKV 98

Séarch completed: Tue Nov 4 10:33:59 1997
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Nov 4 10:30:44 1997; MasPar time 10.73 Seconds 743.322 Million cell updates/sec Tabular output not generated. Run on:

>US-08-842-827-8 (1-276) from USO8842827.pep 2118 1 MQRRWVFULLDVLCLLVASL.....KEEELERRPSLSLTLTLGRG 276 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:annl 2:ann2 3:ann3 4:ann4 5:unannl 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev Database:

Mean 46.202; Variance 109.118; scale 0.423 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

& Query			1			
Score Match Length DB	Length DB	8		a a	Description	Pred. No
6.8	274 11	H		869561	hypothetical protein	1.31e-05
144 6.8 289 11	289 11	11		S70114	hypothetical protein	1.76e-05
112 5.3 317 10	317 10	10		D64233		1.44e-01
5.1	366 4	4		SZBSSE	-3	5.27e-01
108 5.1 596 11	596 11	Ξ		S46001	probable amino acid	4.08e-01
5.0	386 4	4		LABERJ	latent membrane prot	8.76e-01
103 4.9 332 1(332 10	Ä	_	I39800	catabolite control p	1.45e+00
4.9	367	٠.	_	523349	hypothetical protein	1.45e+00
4.9	373 11	급		S19402	hypothetical protein	1.45e+00
6.4	477 13	Ξ		S01696	gene P3 protein - hu	1.45e+00
103 4.9 615 16	615 16	16		066698	YKR106w homolog YCL0	1.45e+00
4.9	615 13	H	_	S40624	hypothetical protein	1.45e+00
8.4	188	-	m	S12686		2.38e+00
4	381 8	ω	_	S24611	latent membrane prot	3.04e+00
4.6	404	4	_	LABECA	latent membrane prot	6.28e+00
₹.	404 8	æ	_	S21660	latent membrane prot	6.28e+00
4.6	616 13	H	~	S64156	probable membrane pr	6.28e+00
4.6	638 13	H	~	177912		6.28e+00
97 4.6 692 13	692 1	H	~	IS7956	glycine transporter	6.28e+00
95 4.5 2016	2016	•	7	A38195	sodium channel prote	1.01e+01
95 4.5 2019	2019		^	A33996	sodium channel prote	1.01e+01

	1.28e+01	1.28e+01	1.61e+01	1.28e+01	1.28e+01	1.28e+01	1.28e+01	1.61e+01	1.28e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.28e+01	٠	2.03e+01	2.03e+01	2.03e+01	2.03e+01	
	tumor necrosis facto	tumor necrosis facto	sodium-dependent pho	ccpA protein - Bacil	cytochrome d complex	latent membrane prot	muscarinic acetylcho	outer capsid protein	amidase (EC 3.5.1.4)	nitrogenase C (nifC)	glycine transporter	glycine transport pr	protein kinase SWEI	thiazide-sensitive e	DNA-directed DNA pol	DNA polymerase delta	sodium channel prote	cadmium resistance p	tumor necrosis facto	muscarinic acetylcho	muscarinic acetylcho	lactoferrin binding	DNA-directed DNA pol	
S52715	\$24642	A25451	£64378	515318	B38170	OQBE50	A35546	S18762	JS0633	H64049	158140	JH0673	S40400	A47296	S17330	A45639	A60165	S51863	S13114	C29514	S33776	I64084	S23019	
14	9	v	10	10	ω	4	13	4	Ŋ	σ	14	^	17	12	12	12	12	1	Ø	14	14	σ	Ŋ	
œ	3	E	σ	334	~	œ	g	C	545	S	'n	3	819	22	1093	60	1321	1515	233	478	479	758	882	
4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4		•	4.3	4.3	4.3	4.3	
94	94	94	66	94	94	94	94	93	94	93	93	93	93	93	93	93	93	94	92	92	92	85	92	
22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; Bult, C.J.; Kerlavage, A.R.; Sutton, G.; Kelley, J.W.; Fritchman, J.L.; Weidman, J.F.; Small, K.V.; Sandusky, M.; Fuhrmann, J.; Wquyen, D.; Utterback, T.R.; Sandusky, D.M.; Phillips, C.A.; Merrick, J.W.; Tomb, J.F.; Dugherty, B.A.; Bott, K.F.; Hu, P.C.; Lucier, T.S.; Peterson, S.N.; Smith, H.O.; Hutchison III, C.A.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neither nucleotide sequence nor conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 drcqpveglpld-tlftakd-vcttknherlldgfrttp-sghssesfaglgylyfwlcg 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D64233 #type complete
hypothetical protein MG302 - Mycoplasma genitalium (SGC3)
hypothetical protein MG302 - Mycoplasma genitalium
#formal_name Mycoplasma genitalium
10.Nov-1995 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 isillavifkllptvkseiirikqaqatrgfiynkcsflnpfkiktlfipvllstvkkte 226
                                                                                                                                                                                                                                                                                                        Score 144; DB 11; Length 289;
Pred. No. 1.76e-05;
65; Mismatches 92; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 19 ledvf-lliimillnypvyygqpferqfyindltishpy-a-tter-vnnnmlfvysfv- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LLDVICLLVASLPFAILTLVNAPYKRGFYCGDDSIRYPYRPDTITHGLMAGVTITATVIL 68
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The minimal gene complement of Mycoplasma genitalium
                                                                                                                                                                                                                                                          *length 289 *molecular-weight 33514 *checksum 4703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length 317 #molecular-weight 36667 #checksum 8963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 qlltesplmplwrkmvaflpllgaal-ialsrtqdyrhhfvdvilgsmlgyima 239
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                                        Fulton, L. submitted to the EMBL Data Library, May 1996 The sequence of S. cerevislae cosmid 9819. 870114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-377 ##label TIGR
##cross-references GB:L43967; TIGR:MG302
##experimental_source strain G-37
                                                                                                                                       ##molecule_type DNA
##residues 1-289 ##label FUL
                                                                                                                                                                                       ##cross-references EMBL:U51031
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Best Local Similarity 24.8%;
Matches 58; Conservative
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Bugalchuk, U.D.; Piggot, P.J.
J. Gen. Microbiol. (1986) 132:1883-1890
Nucleotide sequence of the Bacillus subtilis developmental
                                                                                                                                                                                                                                                                                Kobayashi, Y.

#journal Nucleic Acids Res. (1990) 18:4021

#title Revised nucleotide sequence of the sporulation gene spoVE from Bacillus subtilis.

#cross-reference MUD:90326557

#accession S10243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniel, R.A.; Errington, J.
J. Gen. Microbiol. (1993) 139:361-370
DNA sequence of the murE-murD region of Bacillus subtilis
168.
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                                                                                                                                                                                 06-Jan-1995 #text_change
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#length 366 *molecular-weight 40132 #checksum 1239
                                                                                                                    stage V sporulation protein E · Bacillus subtilis spove protein #formal_name Bacillus subtilis 28-Dec-1997 #sequence_revision 06-Jan-1995 #text_06-Jan-1995
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                                                                                                                                                                                                                                                                 Sato, T.; Theeragool, G.; Yamamoto, T.; Okamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 366;
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Pred. No. 5.27e-01;
25; Mismatches 35; Indels
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##molecule_type DNA
##residues 'MVQIADGYLLFPS',87-366 ##label BUG
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##residues 1-40 ##label DAN
##cross-references NCBIN:125659; NCBIP:125665
                                                                                                                                                                                                                     S10243; A29756; E47691; S22211
S10243
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                                                                                                     *type complete
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##residues 1-366 ##label SAT
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NCE A29756
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#cross-references MUID:87085411
#accession A29756
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Best Local Similarity 22.6%;
Matches 19; Conservative
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#title
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#title Sequence analysis of Raji Epstein-Barr virus DNA.
#cross-references MUID:88219520
#accession C28918
                                                                               1-386 ##label HAT
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Best Local Similarity 26.2%;
Matches 22; Conservative
                                                                                                                  90/1; 118/3
                                                                                                                                                                                                                                                                                                                                                                161 ggnwwtllvdll 172
                                                                                                                                                                                                                                                                                                                                                                                                     219 KHHWSDVLVGLL 230
                                      #accession C28918
##molecule_type_DNA
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Yeast (1994) 10(Suppl.A):S1-S11
The sequence of 29,7kb from the right arm of chromosome II reveals 13 complete open reading frames, of which ten
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Hatfull, G.; Bankier, A.T.; Barrell, B.G.; Farrell, P.J.
Virology (1988) 164:334-340
                                                                                                                                                                                                                       submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain transmembrane *status predicted #label TWZ
#domain transmembrane *status predicted #label TWG
#domain transmembrane *status predicted #label TWI
                                                                                                                                                                                     Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.;
    probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae)
hypothetical protein YBR1007
#formal_name Saccharomyces cerevisiae
6.5-Mag-1994 *sequence_revision 09-Sep-1994 *text_chang
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NCE $46569
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Best Local Similarity 25.7%;
Matches 26; Conservative
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Wang, L.; Romana, L.K.; Reeves, P.R.
Genetics (1992) 130:429-443
Molecular analysis of a Salmonella enterica group El rfb gene
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Hueck, C.; Kraus, A.; Hillen, W.D.R.

Gene (1994) 143:147-148

Sequences of ccpA and two downstream Bacillus megaterium genes with homology to the motAB operon from Bacillus subtilis.
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#formal_name Bacillus megaterium
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
13-Jul-1996
#superfamily Epstein-Barr virus latent membrane protein
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submitted to the Protein Sequence Database, March 1992
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#journal Nucleic Acids Res. (1988) 16:9527-9543
#1111e CpG 1slands of the X chromosome are gene associated.
#cross references MUID:89041548
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S69990 *type complete

YKR106w homolog YCL070/73c - yeast (Saccharomyces cerevisiae)
**Leformal_mame Saccharomyces cerevisiae
05-Dec-1996 *sequence_revision 05-Dec-1996 *text_change
05-Dec-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast (1996) 12:583-591 subtelomeric duplications in Saccharomyces cerevisiae chromosomes III and XI: topology, arrangements, corrections of sequence and strain-specific polymorphism.
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                                                       9
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Gromadka, R.; Gora, M.; Zielenkiewicz, U.; Slonimski, P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 eimsaqfdslkykil-listafvcgfgisldytlrstytgyatnsysehsllstvqvina 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 eimsaqfdslkykil-listafvcgfglsldytlrstytgyatnsysehsllstvqvina 105
                                                                                                                                     276 llggdvtlaismtflstvaatgflplssaiysrllsihetlhvpiskilgtllf-1a1pi 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 DVLCLLVASLPFAILTLVNAPYKRGF-YCGDDSIR--YP-YRPDIIT-HGLMAGVTITAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 DVLCLLVASLPFAILTLVNAPYKRGF-YCGDDSIR--YP-YRPDTIT-HGLMAGVTITAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $40624 *type complete
hypothetical protein YCO70C homolog YKR106w - yeast
(Saccharomyces cerevisiae)
*formal_name Saccharomyces cerevisiae
*formal_name Saccharomyces cerevisiae
03.May-1994 *sequence_revision 03.May-1994 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #map_position 11R
SUMMARY #length 615 #molecular-weight 68953 #checksum 2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #checksum 9357
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  Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103; DB 16; Length 615
Pred. No. 1.45e+00;
34; Mismatches 33; Indels
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Pred. No. 1.45e+00;
34; Mismatches 33; Indels
                                                    30; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status preliminary
##residues 1-615 #label GRO
##coss-references EMBL:X19720
##cross-references FMBL:X #molecular-weight 68897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 vvsvgsqvvysrlsdh-fgrlrlf-lvatifyimgtii 141
Score 103; DB 13;
Pred. No. 1.45e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 VILVSAGEAYLVYTDRLYSRSDFNNYVAAVYKVLGTFL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##experimental_source strain S288C
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                                                                                                                                                                                                          335 avgvliksklpkfsglllgvvkp 357
                                                                                                                                                                                                                                              :: | | :: :: :| | | 111 SLIDLAKYMIGRLKPNFLAVCDP 133
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Best Local Similarity 23.5%;
Matches 23; Conservative
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Best Local Similarity 23.5%;
Matches 23; Conservative
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#authors Hu, L.F.; Zabarovsky, E.R.; Chen, F.; Cao, S.L.; Ernberg, I.; #authors Hu, L.F.; Zabarovsky, E.R.; Chen, F.; Cao, S.L.; Ernberg, I.; #journal Gen. Virol. (1991) 72:2399-2409
#title Isolation and sequencing of the Epstein-Barr virus BNLF-1 gene (LMP1) from a Chinese nasopharyngeal carcinoma. #ccoss-references MUID:92013956
#accession JQ1434
                                                                                                                                                                                                                                                                                                                                                           the authors translated the codon AAA for residue 358 as Ala
                         LABECA #type complete
latent membrane protein - human herpesvirus 4 (strain CAO)
#formal_name human herpesvirus 4, Epstein-Barr virus
31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
09-Sep-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 alylgivlf-ifgcllvfgiwiyfleil-wrlgatlwgllafil-afflaiilliialyl 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 SFYSGHSSFGMY-CM-VF-LALYVQARICWKWARLLRPTVQFFLVAFALYVGFTRVSDY- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain transmembrane #status predicted #label TMI\
#domain transmembrane #status predicted #label TM2\
#domain transmembrane #status predicted #label TM3\
#domain transmembrane #status predicted #label TM5\
#domain transmembrane #status predicted #label TM6\
#domain transmembrane #status predicted #label TM6\
#region II-residue repeats (P-D-N-T-D-D-N-G-D-D)
#length 404 #molecular-veight 43769 #checksum 7535
                                                                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily Epstein-Barr virus latent membrane protein transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: Tue Nov 4 10:32:01 1997
                                                                                                                                                                                                                                                                                                                                          1-404 ##label HUL
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Best Local Similarity 29.2%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       LMP1; BNLF-1
90/1; 119/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 KHHWSDVLVGLL 230
                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
                                                                                                                                            JQ1434
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                                                                                                                                                                                                                                                                                                                                          ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
25-45
51-71
76-97
104-124
140-160
166-186
256-332
                         15
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                                                                                                                                            ACCESSIONS
                                          ENTRY
TITLE
ORGANISM
DATE
                                                                                                                                                                 REFERENCE
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                         RESULT
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                                                                                                                                                                                                                                                                           Ding, S.W.; Howe, J.; Mackenzie, A.; Skotnicki, M.; Gibbs, A. Nucleic Acids Res. (1990) 18:6138
Nucleotide sequence of the virion protein gene of belladonna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           the authors translated the codon ACC for residue 64 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 alylgivlf-ifgcilvlglwiyleilwrlgatiwqllafil-afflaiilliialylqq 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 SFYSGHSSFGMY-CMVFLALXVQARLCWKWARLLRPTVQFFLVAFALXVGYTRVSDY-KH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 qfeatsvgvyetlag-v-nlsssdslakltsgyrrakvvelfltitptgra-idcpvtvd 93
                                                                                                                           S24611 #type complete
tent membrane protein - human herpesvirus 4
#formal_name human herpesvirus 4, Epstein-Barr virus
20-Feb-1995 *sequence_revision 20-Feb-1995 #text_change
12-Apr-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and ACA for residue 167 as U **superfamily turnip yellow mosaic virus coat protein *!ength 188 **molecular-weight 19891 *checksum 5832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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*superfamily Epstein-Barr virus latent membrane
*length 381 *molecular-weight 41372 *checksum
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Pred. No. 2.38e+00;
28; Mismatches 30; Indels
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Pred. No. 3.04e+00;
21; Mismatches 27; Indels
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                                                                                                                    #type complete
.n - belladonna mottle virus
106 vvsvgsgvvysrlsdh-fgrlrlf-lvatifyimgtii 141
                         |: |: | :| :| :| :| :| 6 VILVSAGEAYLVYIDRLYSRSDFNNYAAVKKVLGTFL 103
                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
##residues 1-188 ##label DIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-381 ##label CHA
##cross-references EMBL:X66863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 vawv-panstappskilslyggg 115
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146 LEKVCRGNPADVTEARLSFYSGH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:X54529
                                                                                                                                                                                                                                                                                                                                      mottle tymovirus *cross-references MUID:91045090
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Best Local Similarity 24.1%;
Matches 20; Conservative
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Best Local Similarity 25.7%;
Matches 18; Conservative
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SUMMARY
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                                                                                                                                                                                                                                     ACCESSIONS
REFERENCE
#authors
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ORGANISM
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Score 97; DB 4; Length 404; Pred. No. 6.28e+00; 18; Mismatches 26; Indels

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Nov 4 10:29:23 1997; MasPar time 7.58 Seconds 772.348 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-842-827-8 (1-276) from USO8842827.pep 2118 1 MORRWVFVLLDVLCLLVASL......KEEELERKPSLSLTLTLGRG 276 Description: Perfect Score: Title:

PAM 150 Gap 11 Scoring table:

Sequence:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Database:

Mean 48.002; Variance 91.621; scale 0.524 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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٠.	Pred. No	2.95e-67	1.65e-02	7.74e-02	5.70e-02	1.42e-01	2.57e-01	2.57e-01	2.57e-01	2.57e-01	8.29e-01	1.10e+00	1.47e+00	1.47e+00	1.47e+00	2.57e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	4.47e+00
	Description	HYPOTHETICAL 39.0 KD	HYPOTHETICAL PROTEIN	STAGE V SPORULATION P	HYPOTHETICAL AMINO-AC	LATENT MEMBRANE PROTE	GLUCOSE-RESISTANCE AM	P3 PROTEIN.	HYPOTHETICAL 68.9 KD	HYPOTHETICAL 69.0 KD	PROBABLE ABC TRANSPOR	HYPOTHETICAL 27.9 KD	LATENT MEMBRANE PROTE	HYPOTHETICAL 72.6 KD	SODIUM- AND CHLORIDE-	SODIUM CHANNEL PROTEI	TUMOR NECROSIS FACTOR	TUMOR NECROSIS FACTOR	GLUCOSE-RESISTANCE AM	LATENT MEMBRANE PROTE	MUSCARINIC ACETYLCHOL	NATURAL RESISTANCE-AS	SODIUM- AND CHLORIDE-
SOMESKIES	ID	YSX3_CAEEL	Y302_MYCGE	SP5E_BACSU	YBY 2_YEAST	LMP1_EBVR	CCPA_BACME	P3_HUMAN	YCHO_YEAST	YK86_YEAST	YOCH_BACSU	YV23_MYCLE	LMP1_EBVC	YGO2_YEAST	NTGL_HUMAN	CINS_RAT	TNFA_BOVIN	TNFA_RABIT	CCPA_BACSU	LMP1_EBV	ACM4_CHICK	NRM1_CHICK	NTGL_RAT
	DB	ដ	10	6	11	Ø	۲,	7	11	1	11	Ξ	ø	11	ø	7	0	σ	~	ø	Н	9	9
	Length	341	317	366	296	386	332	477	615	615	309	261	404	616	692	2019	233	235	334	386	490	555	633
ф	Query Match	21.8	5.3	5.1	5.1	5.0	4.9	6.4	6.4	4.9	4.7	4.6	4.6	4.6	4.6	4.5	4 . 4	4.4	4.4	4.4	4.4	4.4	4.4
	Score	461	112	107	108	105	103	103	103	103	66	98	97	97	76	95	94	94	94	94	94	94	63
	Result No.	1	7	٣	4	S	9	7	80	σ	10	1	12	13	14	15	16	17	18	19	20	21	22

4 4 47e+00 4 4 47e+00 3 3 39e+00 7 68e+00 7 68e+000 7 68e+000 7 68e+000 7 68e+000 7 68e+000 7 68e+000 7 68e+000 7 68e+00	5.87e+00 7.68e+00 7.68e+00 7.68e+00 1.00e+01
MITOSIS INHIBITOR PRO THIAZIDE-SENSITIVE SO DNA POLYMERSED DELTA METAL RESISTANCE PROT TUMOR NECROSIS FACTOR TUMOR NECROSIS FACTOR 2-HYDROXYMUCONIC SEMI NADH-UBIQUINONE OXIDO OLIGOPEPTIDE TRANSPOR PREPROTEIN TRANSLOCAS MUSCARINIC ACETYLCHOL M	PRODABLE TONB-DEPRNDE PROBABLE PHOSPHATIDYL DNA POLYMERASE I (EC ATP-DEPENDENT PERMEAS ANTIGEN WO1.1. PROTEIN-TYROSINE PHOS
SWEL YEAST TSCC_PSEAM DEDD_PLARK YCEL YEAST YMI7_MARPO TWRA_CEREL TWRA_CEREL DMPD_PSEPU NUZM_PISOC OPPB_MYCGE SECY_SULAC ACM4_RAIT ACM4_	Y661_HABIN MSS4_YEAST DPO1_SULSO HST6_CANAL WC11_BOVIN ROLB_AGRRB
	10 10 10 8
819 1023 1023 10194 1515 229 229 229 234 283 353 353 463 479 479 479	758 779 882 1323 1436 262
चित्रच्चत्वचचचचचचचचचचच चचचचचणणणणणणणणणणणणणणणणणणणणण	. 4 4 4 4 4 4
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	000000000000000000000000000000000000000
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	

ALIGNMENTS

RESULT ID Y AC Q	TLT 1 YSX3_CAEEL Q10022;	STA	STANDARD;	ä	PRT;	341	1 AA	•						
5555	01-0CT-1996 01-0CT-1996 01-0CT-1996	(REL. (REL. (REL.	34,	CREATED) LAST SEC	34, CREATED) 34, LAST SEQUENCE UPDATE) 34, LAST ANNOTATION UPDATE)	E UPD	ATE) PDAT	. (E)	Ş	;				
N E	T28D9.3.		5	NOTE TO	12009	?	200	200	2	-				
800	CAENORHABDITIS ELEGANS. EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA;	IIS ELE	GANS	; OELOW	ATES: N	EMATOI	D.A.:	SECE	SECERNENTEA	TEA:		RHABDITIDA	4	
R'N	[1]													
д. Б	SEQUENCE FROM N.A	OM N.A.												
א א א	STRAIN-BRISTOL NZ; WATERSTON R .	(ZE NZ)												
H 12	SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS	JUN-195	5) I	O EMB1	/GENBA	NK/DDI	BJ D	ATA	BANK	r)				
ខ	-! - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN	JLAR LC	CATI	ON: II	VTEGRAL	MEMB	RANE	PRC	TEIN	8	(POTENTIAL)	AL)		
ပ္ပ	-!- SIMILARITY: WEAK, TO YEAST D9719.9	TY: WE	AK,	TO YE	AST D97	19.9.								
DR	EMBL; U28738; G861267;	3; G861	267;	ď										
E E	WORMPEP; T28D9.3; CE02068	309.3;	CEOZ	. 890										
32	HYPOTHETICAL PROTEIN; TRANSMEMBRANE.	PROTE	NIN;	TRANS	JEMBRAN	Ξ.								
E E	TRANSMEM	9 30	20	_	POTEN	POTENTIAL.								
E 1	TRANSMEM	7;	5		POTEN	TIAL.								
E E	TRANSMEM	122	142	•• -	POTENTIAL	TIAL.								
į	TONICHEM	247	4 6		DOMENTAL	112								
S		341 AA;	4	39028 MW	٠.	89AE6E81	CRC	CRC32;						
ರಣ	Query Match			21.8%;	Score 461;	461; DB 11;	DB	ij		Length	341;			
ž		similarity 30.1% 93; Conservative	5	1. V.	63; Mismatches	No. Z ismat	ches	94;		Indels		15; G	Gaps	14
Db	21 grskqf	jislfi1	flat	aavtv	qrskqfgislfifflataavtvivptllgvs-qrgffcdddsiryeyrkdtitavglmly	vs-qr	gffc	gppp	irye	yrkd	tita	'qlml	7	On
δy	2 ORRWVF	-VLLDVI	CLLV	ASLPF	QRRWVF-VLLDVLCLLVASLFFAILTLVNAPYKRGFYCGDDSIRYPYRPTIHG-LMA	APYKR	GFYC	5005	IRYP	YRPD	TITH	- K	- 58	m
Ω	80 nlvlnag	atvlfve	2yyru	qkvesı	nlvlnaatylfveyyrmgkvesninnpryrwrnnhlhvlfvrlltyfgysgigfvmnial	rwrnn	hlhv	lfvr.	11ty	fgys	gigf	7mnia		139
δλ	59 GVTI-T#	:: ATVILVS	AGE	: VYLVYTI	: : : :: GVTI-TATVILVSAGEAYLVXTDRLYSRSDF-NNYVAAVY-KVLGTFLFGA-A-VSQ-SL	DE-NN	ii: nnyvaa	:: :: AVYKVL	: l :VLGT	FLFG	A-A-1	7SQ-S		112
qq	140 nivtkh	vgrlrį	h£1ć	lvckla	nivtkhvvgrlrphfldvcklandtcvtgdshryit-dytctgppelvlearksfysghs	dshry	it-d	lytct	dbpe-	lvle	arks	iysgh		198
δy	::: 113 TDLAKY	: :: AKYMIGRLKPNFLAVCD	: I I	VCD-PI	:: :: : : :: : :: ::	NCSVY	: VQLE	KVCF	GNPA	DVTE	II			169
Сp	199 avslyce	atwsaly	'igar	lygpvl	avslycatwsalyiqarlgpvlnnrivvpisqtlmfmiglgisfsritdnkhhwsdvlvg	isqtl	m£m1	glgi	sfsr	itdn	khhw	sdvlv		258
οy	170 SFGMYCN	- 	VQAE	LCWKW	SEGMYCMVFLALYVQARLCWKWA-RULRPTVQFFLVAFALYVGYTRVSDYKHHWSDVLVG	TVQFF	: LVAF	ALY.	GYTR	VSDY	KHHW	SDVLV		228

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DANIEL R.A., ERRINGTON J.;
J. GEN. MICROBIOL. 139:361-370(1993).

J. GEN. MICROBIOL. 139:361-370(1993).

I. FUNCTION: MAY PLAY AN ESSENTIAL ROLE NOT ONLY DURING SPORULATION,
BUT ALSO DURING VEGETATIVE GROWTH.

I. SUBCELLICHAR LOCATION: INFERRAL MEMBRANE PROTEIN.

I. SIMILARITY: BELONGS TO THE FTSW/RODA/SPOVE FAMILY.

I. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN THE N-TERMINUS

AND IS SHORTER DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 agigviam-ffimnvdywt-wrtwskilm-vicffilvlvlipgvgmvrngsrswigvga 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 SSFGMYCMVFLALYVQARLCWK-WARLLRPTVQFFLVAFALYVGYTRVSDYKHHWSDVLV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISCUSSION OF SEQUENCE.
MEDLINE; 95042830.
NASR F., BECAM A.-M., GRZYBOWSKA E., ZAGULSKI M., SLONIMSKI P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BECAM A.-M., CULLIN C., GRZYBOWSKA E., LACROUTE F., NASR F., OZIER-KALOGEROPOULOS O., PALUCHA A., SLONIMSKI P.P., ZAGULSKI M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1994 (REL. 30, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
HYPOTHETICAL AMINO-ACID PERMEASE IN VMA2-CKSI INTERGENIC REGION.
                                            SEQUENCE OF 1-46 FROM N.A.
THEERAGOOL G., MIYAO A., YAMADA K., SATO T., KOBAYASHI Y.;
SUBMITTED (JAN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107; DB 9; Length 366
Pred. No. 7.74e-02;
25; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
ECC56F98 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        596 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
J. GEN. MICROBIOL. 132:1883-1890(1986).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                   SUBTILIST; BG10226; SPOVE.
PROSITE; PS00428; FTSW_RODA_SPOVE.
SPORULATION; CELL SHAPE; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                EMBL, X51419; G580937; -.
EMBL, M15742; G143657; ALT_FRAME.
EMBL, D14109; G216543; -.
EMBL, 215056; -; NOT_ANNOTATED_CDS.
PIR; A29756; S2BSSE.
PIR; S10243; S10243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 GLLQGALVAALT-VCYISDFFKAR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 fsiqpsefmklamiaflakflsek 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40132 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.1%;
ilarity 22.6%;
Conservative
                                                                                                                SEQUENCE OF 1-40 FROM N.A. STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
70
1125
1164
1264
1264
326
336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EAST 10:S1-S11(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264
306
337
366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YBR132C OR YBR1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C;
MEDLINE; 94378717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 4
YBY2_YEAST
P38090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                             FRASER C.M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,
FLEISCHMANN R.D., BULT C.J., KERLAVGE A.R., SUTTON G., KELLEY J.M.,
RETLICHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRMANN J.L.,
NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M.,
TOMB J.F., DOUGHERPIY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,
SCIENCE 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACILLUS SUBTILIS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 isillavifkilptvkseiirikqaqatrgfiynkcsflnpfkiktlffpvllstvkkte 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VFVLLDVLCLLVASLPFAILTLVNAPYKRGFYCGDDSIRYPYRPDTI-THGLMAGVTITA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                            PROKARYOTA; TENERICUTES; MOLLICUTES; MYCOPLASMA; MYCOPLASMATALES;
MYCOPLASMATACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
EMBL; U39711; G1046001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE; 90326557.
SATO T., THEERAGOOL G., YAMAMOTO T., OKAMOTO M., KOBAYASHI
NUCLEIC ACIDS RES. 18:4021-4021(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 112; DB 10; Length 317
Pred. No. 1.65e-02;
27; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 ttafalqakgydlnntnrthyplkyn-llngvfllvglllfs 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 TVILVSAGEAY-LVYIDRLYSRSDFNNYVAAVYKVLGTFLFG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EF5F2980 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
STAGE V SPORULATION PROTEIN E.
                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                               317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
TRANSMEM 18 38 POTENTI
                                                                                                                                 PRT;
                            259 ifigiflavytctfwtdlfsnnste 283
                                              229 LLOGALVAALTVCYISDFFKARPPQ 253
                                                                                                         1912_MYGGE STANDARD; PR
1912_MYGGE STANDARD;
1947544;
10. FEB-1996 (REL. 33, LAST SEQUE
01. FEB-1996 (REL. 33, LAST SEQUE
01. FEB-1996 (REL. 33, LAST ANNOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1988 (REL. 07, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
MEDLINE; 87085411.
BUGAICHUK U.D., PIGGOT P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.3%;
Best Local Similarity 24.5%;
Matches 25; Conservative
                                                                                                                                                                                                              HYPOTHETICAL PROTEIN MG302 MG302.
                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE; 96026346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
1112
1122
222
272
                                                                                                                                                                                                                                                MYCOPLASMA GENITALIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP5E_BACSU
P07373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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Gaps

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163 SFYSGHSSFGMY-CMVFLAL--YVQARLCWKWARLLRPTVQFFLVAFALYVGYTRVSDY- 218
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (REL. 10,
01-MAR-1989 (REL. 10,
01-OCT-1996 (REL. 34,
                                                                   161 ggnwwtllvdll 172
                                                                                                                                    219 KHHWSDVLVGLL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACILLUS MEGATERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 94259294. HUECK C., KRAUS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89041548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATORS.
                                                                                                                                                                                                                                 LT 6
CCPA_BACME
P46828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 alylgivlf-ifgcilvlglwiylleil-wrlgatiwqllaffl-affldiilliialyl 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPSTEIN-BARR VIRUS (STRAIN RAJI) (HUMAN HERPESVIRUS 4).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                              TRANSPORT; AMINO-ACID TRANSPORT; TRANSMEMBRANE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MADLINE; B8219520.
HATFULL G., BANKIER A.T., BARRELL B.G., FARRELL P.J.;
VIROLOGY 164:334-340(1988).
-I.- FUNCTION: THE LATENT MEMBRANE PROTEIN HAS TRANSFORMING ACTIVITY.
PHB.; M20868; G330381; -.
PIR: C28918; LABERJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
CURR. GENET. 26:1-7(1994).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
PERKEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 105; DB 6; Length 386;
Pred. No. 1.42e-01;
19; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108; DB 11; Length 596
Pred. No. 5.70e-02;
31; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEMBRANE; PHOSPHORYLATION; TRANSFORMING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 ATVILVSAGEAYLVYTDRLYSRSDFN-NYVAAVYKVLGTFL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   514 samili-qg--ytvffpklwntqdflfsylm-vfinigiyv 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206A848D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B73A2587 CRC32;
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01-0AN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
LATENT MEMBRANE PROTEIN 1 (LMP-1) (P63).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 AA.
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POTENTIAL.
CYTOPLASMIC.
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                                                                                                                                                                                                                                                                                       PROSITE; PS00218; AMINO_ACID_PERMEASE HYPOTHETICAL PROTEIN; TRANSPORT; AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Best Local Similarity 29.2%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.1%;
Best Local Similarity 25.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42061
                                                                                                                                                         EMBL; X75891; G496863; -. EMBL; Z36001; G536423; -. PIR; S46001. S46001. PIR; S46575; S46575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             596 AA;
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LMP1_EBVR
P13198;
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PEPERSSION OF CARBOHYDRALE REGULATOR INVOLVED IN BOTH THE REPRESSION OF CARBOHYDRATE UTILIZATION GRRES SUCH AS THE ALPHA-AMYLASE (AMYE) AND THE ACETYL-COENZYME A SYNTHETASE (ACKSA); AND IN THE POSITIVE REGULATION OF GENES INVOLVED IN EXCRETION OF EXCESS CARBON SUCH AS THE ACETALE KINASE (ACKA). MAY PLAY A ROLE IN REGULATION OF CITRATE SYNTHASE GENE EXPRESSION

-1- SIMILARITY: BELONGS TO THE LACIT FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                             PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: THE UBLQUITOUS EXPRESSION AND THE CONSERVATION OF THI
P3 SEQUENCE IN DISTANT ANIMAL SPECIES SUGGEST THAT THE P3 GENE
                                                             01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
GLUCOSE-RESISTANCE AMYLASE REGULATOR (CATABOLITE CONTROL PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHEN E.Y., ZOLLO M., MAZZARELLA R.A., CICCODICOLA A., CHEN C.N., ZUO L., HEINER C., BUROUGH F.W., RIPETTO M., SCHLESSINGER D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, L26052, G415664; -.
PROSITE; PS00356; HTH_LACI_EAMILY.
TRANSCRIPTION REGULATION; REPRESSOR; ACTIVATOR; DNA-BINDING.
DNA_BIND
SEQUENCE 332 Aa; 36644 MW; A174D030 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.9%; Score 103; DB 2; Length 332
26.2%; Pred. No. 2.57e-01;
ative 28; Mismatches 25; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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332 AA.
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NUCLEIC ACIDS RES. 16:9527-9556(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
PRT;
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                                    01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQI
01-OCT-1996 (REL. 34, LAST ANNI
                                                                                                                                                                                                                                                                     HUECK C., KRAUS A., HILLEN W.;
GENE 143:147-148(1994).
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Matches 22; Conservative
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YOGH BACSU
P46339;
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YK86_YEAST
P36173;
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                                                                                                                                                      Gaps
GROMADKA R.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
1- SUBMITARITY: BELONGS TO THE YCL70C/YHL047C/YKR106W FAMILY.
EMBL; X59720; E264591; -
PIR; S19402; S19403.
PIR; S19403; S19403.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.9%; Score 103; DB 11; Length 615;
23.5%; Pred. No. 2.57e-01;
tive 34; Mismatches 33; Indels
                                                                                                          Length 477;
                                                                                                        Score 103; DB 7; Length 477,
Pred. No. 2.57e-01;
30; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                VAN DER AART Q.J.M., STEENSMA H.Y.;
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                               YCHO_YEAST STANDARD; PRT; 615 AA.
P25565 P25597; P25599;
01-MAY-1992 (REL. 22, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
1 HYPOTHETICAL 68.9 KD PROTEIN IN HAL 5'REGION.
YCLO/DC/71C/73C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                               TRANSMEMBRANE; TRANSPORT; SYMPORT.
SEQUENCE 477 AA: 50332 MW; 653D4BA7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
OBBD5B37 CRC32;
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                                                                                                                                                                                               111 SLIDLAKYMIGRLKPNFLAVCDP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568
68898 MW;
                                                                                                        4.9%;
Local Similarity 26.5%;
hes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          larity 23.5%;
Conservative
                                           EMBL; X12458; G35188; -.
EMBL; L44140; G1203976; -.
PIR; S01696; S01696.
MIM; 312090; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
3328
328
424
921
921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                615 AA;
                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
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REVISIONS.
                                   (SBE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
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                                                                                                           Duery Match
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PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 DVLCLLVASLPFAILTLVNAPYKRGF-YCGDDSIR--YP-YRPDTIT-HGLMAGVTITAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)
PROBABLE ABC TRANSPORTER PERMEASE PROTEIN IN SODA-COMGA INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAILLON L., DUJON B.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-1- SIMILARITY: BELONGS TO THE YCL70C/YHL047C/YKR106W FAMILY.
EMBL: Z18202; G486617; -,
PIR: S40624; S40624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
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STRAIN-168 / JH642;
TAKENGHU K., MIZUNO M., SATO T., TAKEUCHI M., KOBAYASHI Y.;
SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-168 / JH642;
STRAIN-184 / JH642;
KOBAYARAI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO : SATO I., TAKEUCHI M.;
SATO I., TAKEUCHI M.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                      Score 103; DB 11;
Pred. No. 2.57e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 vvsvgsgvvysrlsdh-fgrlrlf-lvatifyimgtii 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 vvsvgsgvvysrlsdh-fgrlrlf-lvatifyimgtii 141
                                                                                                                                                                                                                                                                         01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HYPOTHETICAL 69.0 KD PROTEIN IN SIRI 3'REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
A8423CFB CRC32;
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                                                                                                                                                                                                                615
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POTENTIAL.
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POTENTIAL.
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68954 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.9%;
larity 23.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472
549
615 AA;
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es 23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
LATENT MEMBRANE PROTEIN 1 (LMP-1) (P63).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM.
PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS
THE MEMBRANE (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-PROTEIN. DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTW
SUBFRAILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 LMAGVIITATVIL-VSAGEAYLVY-TDRL-YSRS-DFNNYVAAV-YKVLGTFLFGAAVSQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 vvfgaglfvafdgl-wrwnsiv-alvlsvlvilglvvg-vrvvrrtediastliavvvga 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 imiaasvaitiflgvkglqsflvngvspiefltslnwnptdsdpkygvl-pfifgsfavt 96
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SMITH D.R., FROBISON K.;
SMITH D.R., WARN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-- SUBLITITY: STRONG, TO M.TUBERCULOSIS MICY20G9.23.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98; DB 11; Length 261;
Pred. No. 1.10e+00;
16; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Score 99; DB 11; Length 309;
Pred. No. 8.29e-01;
24; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYCOBÄCTĒRIUM LEPRAE.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
                                                                                                                 SUBFAMILY.

EMBL, D58414; G903304; ...

EMBL, D84432; G130355; ...

SUBTILIST; BG11376; YQGH.

PROSITE; PSO0402; BPD_TRANSP_INN_MEMBR.

HYPOTHETICAL PROTEIN: TRANSPORT; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
9712F280 CRC32;
                                                                                                                                                                                                                                                                                                                             POTENTIAL.
ED7700D9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.9 KD PROTEIN B2168_C2_209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 AA.
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                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                               108 PC
153 PC
185 PC
234 PC
300 PC
33219 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 12
LMP12BVC STANDARD;
P29362;
01-DEC-1992 (REL. 24, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 256 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.7%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.7%;
Best Local Similarity 24.1%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
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227
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165
165
214
280
309 AA;
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207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 11
YV23_MYCLE
P54580;
                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 SFYSGHSSFGMY-CM-VF-LALYVQARLCWKWARLLRPTVQFFLVAFALYVGYTRVSDY- 218
EPSTEIN-BARR VIRUS (STRAIN CAO) (HUMAN HERPESVIRUS 4).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE.
                                                     SEQUENCE FROM N.A.

MUDLINE, 20103956.

HU L.F., ZABAROVSKY E.R., CHEN F., CAO S.L., ERNBERG I., KLEIN G., WINBERG G.; AROLLSKY E.R., CHEN F., CAO S.L., ERNBERG I., KLEIN G., TYLOL. 72.2399-2409(1991).

-I- FUNCTION: THE LATERT MENBRANE PROTEIN HAS TRANSFORMING ACTIVITY. EMBL, X59140; G22938; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 9317110.
PEL H.J., MAAT M.J., REP M., GRIVELL L.A.;
PEL H.J., MAAT M.J., REP M., GRIVELL L.A.;
PUCLER: CALIDS RES. 20:6339-6346 (1992).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: SOME, TO S. POWBE SPACZGII.09 AND SPAC4G8.12C.
EMBL; Z72664; E243764;
-:- EMBL; X60381, 288601;
-- PIR; S28601; S28601.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 72.6 KD PROTEIN IN MRF1-SEC27 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97; DB 6; Length 404;
Pred. No. 1.47e+00;
18; Mismatches 26; Indels
                                                                                                                                                                                          PIR: JO1434; LABECA.
PIR: S21660; S21660.
TRANSMEMBRANE; PHOSPHRYLATION; TRANSFORMING PROTEIN.
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
VOLCKAERT G., VOET M., VERHASSELT P., DEFOOR E.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGL142C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA, FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC.
154E84C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    616 AA.
                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (REL. 26, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                   43769 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 339-616 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 4.6%;
Local Similarity 29.2%;
Nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                            447
447
447
408
408
408
408
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359
359
413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 KHHWSDVLVGLL 230
                                                                                                                                                                                                                                                                                                                                                       139
166
187
404 AA;
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P30777;
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16
692 AA;
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CINS_RAT
P15389;
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SVLKVWHGAYNSGLLPQLMAQHSLAMAQ -> MVGKGAKGM
L (IN FORM 1A).
                                                                                                                              87 illhyal-illstigsdllilllpkyelswqvaedlkrlpfdvtrsfeyygviyapkivm 145
                                                                                                                                               GLYT
                                                                                                 Gaps
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TISSUE SPECIFICITY: ALL GLYT-1 SUBTYPES CAN BE FOUND IN BRAIN,
KIDNEY, PANCRRAS, LUNG, PLACENTA, LIVER. BUT GLYT-1C SUBTYPE IS
ONLY FOUND IN THE BRAIN.
ALTERNATIVE PRODUCTS: THREE ISOFORMS (GLYT-1A, GLYT-1B, AND GLYT-1C).
ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING: FORM GLYT-1C IS SHOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIM K.-M., KINGSMORE S.E., HAN H., YANG-FENG T.L., GODINOT N., SELDIN M.F., CARON M.G., GIROS B.; MOL. PHARMACOL. 45:608-617(1994).
-!- FUNCTION: TERMINATES THE ACTION OF GLYCINE BY ITS HIGH AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEUROTRANSMITTER TRANSPORT; TRANSPORT; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITTER SYMPORTER
                                                                                                 9
                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSPORTER 1 (GLYT-1)
                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                  Length 616;
                                                                            Pred. No. 1.47e+00;
22; Mismatches 30; Indels
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                 S -> A (IN REF. 2
CBE29FF0 CRC32;
                                                                DB 11;
                                                                                                                                                                                                                                                                                        692 AA
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                                                                Score 97;
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   444 Po
339 S
72565 MW;
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                                                                                                                                                                                           146 av-lasigeyyivrfvqkly 164
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65 TVILVSAGEAYLV-YTDRLY 83
                                                             Query Match
Best Local Similarity 27.5%;
Matches 22; Conservative
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292
318
371
503
539
424 4
339 3
616 AA;
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NTGL_HUMAN
P48067;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 90046760.

ROGART R.B., CRIBBS L.L., MUGLIA L.K., KEPHART D.D., KAISER M.W.;

PROC. NATL. ACAD. SCI. U.S.A. 86:8170-8174(1989)

-! FUNCTION: THIS PROFERI MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION

-! FUNCTION: THIS PROFERI FOR WELL ACCOMED OR CLOSED

CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTYCE CHANNEL THROUGH

WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL

GRADIENT IT IS A TETRODOTOXIN-RESISTAMT NA+ CHANNEL SOFPOM.

-! NA+ CHANNELS IN MAMMALIAN CRADIACA MERRANE HAVE FUNCTIONAL

PROPERTIES OUITE DISTINCT FROM NA+ CHANNELS IN NERVE AND SKELETAL
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E; ION TRANSPORT; VOLTAGE-GATED CHANNEL; MULTIGENE FAMILY; PHOSPHORYLATION.
                                                                              .:
                                                                                                             610
                                                                                                                              RAȚIUS NORVECICUS (RAI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                             562 w-rfvspaiiffilvftv-iqyqpitynhyqypgwa-vaigflm-alssvlci
                                              Length 692;
                                                                              17; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVERY THIRD POSITION.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
--: SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
EMBL: M37902; G206858; -.
PIR: A33996; A33996.
                                                                                                                                                                                                                                        01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SODIOW CARNNEL PROMEIN, CARDIAC MUSCLE ALPHA-SUBUNIT.
69 MISSING (IN FORM 1B)
76823 MW; 5A5184C7 CRC32;
                                              Score 97; DB 6; L
Pred. No. 1.47e+00;
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REPEAT I.
REPEAT I.
REPEAT I.
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                                              4.6%;
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                                                                              15; Conservative
                                                                                                                                                                                                            STANDARD;
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2277
772
800
800
863
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1226
1265
1293
1319
1472
                                                                Local Similarity
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215 POTENTIAL.
284 POTENTIAL.
289 POTENTIAL.
292 POTENTIAL.
292 POTENTIAL.
319 POTENTIAL.
593 POTENTIAL.
593 POTENTIAL.
594 POTENTIAL.
865 POTENTIAL.
          215
284
289
229
319
329
741
864
865
865
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1367
1380
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865 86
949 94
1367 136
1376 137
1392 138
2019 AA;
     CARBOHYD
CAR
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ä; Gaps 3; Score 95; DB 2; Length 2019; Pred. No. 2.57e+00; 15; Mismatches 16; Indels Query Match
Best Local Similarity 27.7%;
Matches 13; Conservative

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Search completed: Tue Nov 4 10:30:26 1997 Job time: 63 secs.